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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:34:13 : Search time 110.536 Seconds
(without alignments)
922.194 Million cell updates/sec

Title: US-09-847-208b-3
Perfect score: 1260
Sequence: 1 EPKSCDKTHTCPCPAPELL.....MHEALHNYQQRSLSPGK 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Geneseq 21: *
1: geneseqp1980a: *
2: geneseqp1990a: *
3: geneseqp2000a: *
4: geneseqp2001a: *
5: geneseqp2002a: *
6: geneseqp2003a: *
7: geneseqp2003bs: *
8: geneseqp2004a: *
9: geneseqp2005a: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260	100.0	232	AA019665	AA019665 Human IgG
2	1260	100.0	330	AA019664	AA019664 Human IgG
3	1260	100.0	569	AA019668	AA019668 GE2 fusio
4	1232	97.8	232	AD287506	AD287506 Human IgG
5	1228	97.5	330	AD269628	AD269628 Human IgG
6	1225	97.2	232	AAW26232	AAW26232 Human IgG
7	1225	97.2	232	AAE28690	AAE28690 Human IgG
8	1225	97.2	232	AAE80897	AAE80897 Human IgG
9	1225	97.2	232	AAE72915	AAE72915 Human par
10	1225	97.2	232	AAE15347	AAE15347 Human imm
11	1225	97.2	232	AAE26272	AAE26272 Human IgG
12	1225	97.2	232	ADJ65991	ADJ65991 Herpes vi
13	1225	97.2	232	ADJ57512	ADJ57512 Human IgG
14	1225	97.2	232	ADR48992	ADR48992 Human IgG
15	1225	97.2	232	ADU51146	ADU51146 Human sp1
16	1225	97.2	232	ADW39127	ADW39127 Novel TNF
17	1225	97.2	232	ADV91799	ADV91799 Human GCS
18	1225	97.2	232	ADV99720	ADV99720 Human IgG
19	1225	97.2	232	ADY55884	ADY55884 Human IgG
20	1225	97.2	232	ADZ86538	ADZ86538 Human IgG
21	1225	97.2	232	AEA18941	AEA18941 Human IgG
22	1225	97.2	232	AEA88761	AEA88761 Human IgG
23	1225	97.2	233	ABB09463	ABB09463 Human IgG
24	1225	97.2	234	ADY22146	ADY22146 Human imm

25	1225	97.2	235	6	ABJ38647	ABJ38647 pCXFc pro
26	1225	97.2	235	6	ADA89055	ADA89055 Plasmid p
27	1225	97.2	235	7	ADD25647	ADD25647 Binding d
28	1225	97.2	235	7	ADG74307	ADG74307 Fibroblas
29	1225	97.2	235	9	ADY21627	ADY21627 Human IgG
30	1225	97.2	247	5	AAE26274	AAE26274 Human bet
31	1225	97.2	251	5	ABB81490	ABB81490 Human imm
32	1225	97.2	251	6	AAE35214	AAE35214 Human wil
33	1225	97.2	259	2	AAE24154	AAE24154 Protein f
34	1225	97.2	267	5	AAE26273	AAE26273 Human tPA
35	1225	97.2	269	8	ADJ52120	ADJ52120 CHI delet
36	1225	97.2	285	9	AEA89551	AEA89551 Human imm
37	1225	97.2	287	4	AAE47590	AAE47590 Fusion pr
38	1225	97.2	288	9	AEA89541	AEA89541 Human imm
39	1225	97.2	329	2	AAE91806	AAE91806 Human imm
40	1225	97.2	329	8	ADP56389	ADP56389 Human PRO
41	1225	97.2	329	8	ADS82579	ADS82579 Human IgG
42	1225	97.2	330	4	AAE04071	AAE04071 Zcytor 10
43	1225	97.2	330	5	AAE47856	AAE47856 Human Ig-
44	1225	97.2	330	5	AAE21960	AAE21960 Human dea
45	1225	97.2	330	5	ABB81641	ABB81641 Human IgG

ALIGNMENTS

RESULT 1
AA019665
ID AA019665 standard; protein; 232 AA.

XX	AC	AA019665;
XX	DT	28-MAR-2003 (first entry)
XX	DE	Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.
XX	KW	Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
XX	KW	Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
XX	KW	antiasthmatic; antiallergic; antiinflammatory; dermatological;
XX	KW	antiarthritic; antirheumatic; antidiabetic; neuroprotective;
XX	KW	hinge-CH2-CH3 region.
XX	OS	Homo sapiens.
XX	FN	WO200288317-A2.
XX	PD	07-NOV-2002.
XX	PF	01-MAY-2002; 2002WO-US013527.
XX	PR	01-MAY-2001; 2001US-00847208.
XX	PR	24-OCT-2001; 2001US-00000439.
XX	XX	(REGC) UNIV CALIFORNIA.
XX	PI	Saxon A, Zhang K, Zhu D;
XX	XX	WPI; 2003-103456/09.
XX	DR	New fusion molecules comprising polypeptide sequences that bind to IgG
XX	PT	inhibitory receptor and native IGE receptor, useful for treating IGE-
XX	PT	mediated hypersensitivity reactions, e.g. asthma or allergies, or
XX	PT	autoimmune diseases.
XX	PS	Claim 19; Fig 3; 116pp; English.
XX	CC	The present invention relates to a fusion molecule comprising a first
XX	CC	polypeptide sequence capable of specific binding to a native IgG
XX	CC	inhibitory receptor consisting of an immune receptor tyrosine-based
XX	CC	inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
XX	CC	functionally connected to a second polypeptide sequence capable of
XX	CC	specific binding directly or indirectly to a native IGE receptor
XX	CC	(Fc epsilonR). Also provided are nucleotide sequences encoding such a

CC fusion protein. The fusion molecules and compositions are useful for
CC treating an IGE-mediated biological response, preferably an IGE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgG1
CC heavy chain constant region hinge-CH2-CH3 portion
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 1260; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.3e-91;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

RESULT 2
AAO19664
ID AAO19664 standard; protein; 330 AA.
XX AAO19664;
XX
XX 28-MAR-2003 (first entry)
XX Human IgG1 heavy chain constant region.

XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
KW Fcεpsilon receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; anti-allergic; anti-inflammatory; dermatological;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.
XX Homo sapiens.
XX WO200288317-A2.
XX 07-NOV-2002.
XX 01-MAY-2002; 2002WO-US013527.
XX 01-MAY-2001; 2001US-00847208.
XX 24-OCT-2001; 2001US-00000439.
XX (REGC) UNIV CALIFORNIA.
XX Saxon A, Zhang K, Zhu D;
XX WPI; 2003-103456/09.
XX New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IGE receptor, useful for treating IGE-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX Claim 64; Fig 2; 116pp; English.
XX The present invention relates to a fusion molecule comprising a first

CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IGE receptor
CC (FcεpsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC treating an IGE-mediated biological response, preferably an IGE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgG1
CC heavy chain constant region
XX

SQ Sequence 330 AA;
Query Match 100.0%; Score 1260; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.1e-91;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120
DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQORSLSLSPGK 330

RESULT 3
AAO19668
ID AAO19668 standard; protein; 569 AA.
XX AAO19668;
XX AAO19668;
XX 28-MAR-2003 (first entry)
XX GE2 fusion protein for use in treating immune diseases.
XX Human; IgE; immunoglobulin E; immunotherapy; immune disease;
KW Fcεpsilon receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; anti-allergic; anti-inflammatory; dermatological; GE2;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
KW fusion protein.
XX Synthetic.
OS Unidentified.
XX WO200288317-A2.
XX 07-NOV-2002.
XX 01-MAY-2002; 2002WO-US013527.
XX 01-MAY-2001; 2001US-00847208.
XX 24-OCT-2001; 2001US-00000439.
XX (REGC) UNIV CALIFORNIA.
XX Saxon A, Zhang K, Zhu D;
XX WPI; 2003-103456/09.
XX

PT New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IgE receptor, useful for treating IgE-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX
XX
XX Claim 35; Fig 7; 116pp; English.
XX
XX The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IgE receptor
CC (FcpsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC treating an IgE-mediated biological response, preferably an IgE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type 1 hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is a gammahinge-
CC CHgamma2-CHgamma3-(Gly4Ser)3-CHepsilon2-CHepsilon3-CHepsilon3 fusion
CC protein (designated GE2) of the invention
XX
XX Sequence 569 AA;

Query Match 100.0%; Score 1260; DB 6; Length 569;
Best Local Similarity 100.0%; Pred. No. 9.7e-91;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNKGKEYCKKYSNKKALPAPIETK 120
DB 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNKGKEYCKKYSNKKALPAPIETK 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVMEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVMEALHNHYQOQSLSLSPGK 232

RESULT 4
ADZ87506
ID ADZ87506 standard; protein; 232 AA.
XX
XX ADZ87506;
XX
XX 14-JUL-2005 (first entry)
XX
XX Human IgG1 protein region SeqID33.
XX
XX protein engineering; immunoglobulin; cytostatic; cancer.
XX
XX Homo sapiens.
XX
XX WO2005042573-A1.
XX
XX 12-MAY-2005.
XX
XX 21-OCT-2004; 2004WO-US034680.
XX
XX 24-OCT-2003; 2003US-0514198P.
XX
XX 12-NOV-2003; 2003US-0519822P.
XX
XX (DAND) DANA FARBER CANCER INST INC.
XX (ILEX-) ILEX PROD INC.

XX
XX
XX Kharbanda S, Kufe DW;
XX WPI; 2005-346855/35.
XX N-PSDB; ADZ87507.
XX
XX MUC1 ligand trap comprising a MUC1 extracellular polypeptide and an
PT immunoglobulin FC polypeptide or an albumin polypeptide, useful for
PT treating cancer.
XX
XX Disclosure; SEQ ID NO 33; 82pp; English.
XX
XX This invention relates to a novel MUC1 chimeric protein which comprises a
CC first polypeptide sequence and a second polypeptide sequence, where the
CC first polypeptide sequence is a MUC1 extracellular (MUC1-EC) polypeptide,
CC and the second polypeptide sequence is a human immunoglobulin FC
CC polypeptide or a human albumin polypeptide. The invention may be useful
CC for the development of compounds with a cytostatic activity acting as
CC MUC1 antagonists or CD227 antagonists. The MUC1 chimeric protein is
CC useful in preparing a composition for treating cancer. The present
CC sequence is that of a protein which was used during the development of
CC the novel MUC1 chimeric protein of the invention.
XX
XX Sequence 232 AA;

Query Match 97.8%; Score 1232; DB 9; Length 232;
Best Local Similarity 97.4%; Pred. No. 5.4e-89;
Matches 226; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNKGKEYCKKYSNKKALPAPIETK 120
DB 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNKGKEYCKKYSNKKALPAPIETK 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVMEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVMEALHNHYQOQSLSLSPGK 232

RESULT 5
ADZ69628
ID ADZ69628 standard; protein; 330 AA.
XX
XX ADZ69628;
XX
XX 14-JUL-2005 (first entry)
XX
XX Human IgG1 heavy chain constant region, mutant L314M.
XX
XX Heavy chain constant region; antibody engineering; protein engineering;
XX immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasia;
XX autoimmune disease; immunosuppressive; immune disorder.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 197
XX /note= "Wild-type Leu substituted by Met"
XX
XX WO2005037867-A1.
XX
XX 28-APR-2005.
XX
XX 15-OCT-2004; 2004WO-US034440.
XX

PR 15-OCT-2003; 2003US-0511687P.
PR 14-APR-2004; 2004US-0562627P.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Hinton PR, Tsurushita N;
XX WPI; 2005-315683/32.
XX
XX New modified Fc-fusion protein where at least one amino acid residue from
PT the heavy chain constant region, useful for studying protein function in
PT vitro and in vivo and as potential therapeutic and diagnostic agents.
XX
XX Claim 21; SEQ ID NO 29; 170pp; English.
XX
XX The invention relates to a modified Fc-fusion protein where at least one
CC amino acid residue from the heavy chain constant region selected from
CC residues 250, 314, and 428 (Kabat numbering) is different from that
CC present in the unmodified Fc-fusion protein. Also included are an Fc-
CC fusion protein comprising an Fc region substantially identical to that of
CC a naturally occurring class IgG antibody, a modified Fc-fusion protein
CC with an in vivo mean elimination half-life at least about 1.3-fold longer
CC than that of the corresponding unmodified Fc-fusion protein, a modified
CC IgG class antibody fragment (comprising a heavy chain constant region or
CC Fc-region where at least one amino acid residue selected from the group
CC consisting of residues 250, 314, and 428 is different from that present
CC in the unmodified IgG class antibody), an isolated polynucleotide
CC molecule encoding a polypeptide comprising a sequence at least 90%
CC identical to a sequence selected from ADZ69600-ADZ69656, an isolated
CC polypeptide comprising an amino acid sequence at least 90% identical to a
CC sequence selected from ADZ69600-ADZ69656, a method for altering FcRn
CC binding affinity/serum half-life of an Fc-fusion protein (comprising
CC selecting at least one amino acid residue as cited above, and
CC substituting the selected residue(s) with an amino acid different from
CC that present in the Fc-fusion protein) and a method of producing a
CC modified Fc-fusion protein with an altered binding affinity for
CC FcRn/alterd serum half-life as compared with the unmodified Fc-fusion
CC protein (comprising preparing an expression vector comprising a suitable
CC promoter operably linked to DNA encoding at least a constant region of an
CC IgG heavy chain, transforming host cells with the vector and culturing
CC the transformed host cells to produce the modified IgG Fc fusion
CC protein). The modified antibody has a higher affinity for FcRn at pH 6.0
CC than at pH 8.0. The fusion proteins are useful for studying protein
CC function in vitro and in vivo and as potential therapeutic and diagnostic
CC agents. The present sequence represents a human IgG1 heavy chain constant
CC region with an amino acid substitution at residue 250, 314 or 428 (Kabat
CC numbering, the actual residue that is mutated is covered in the feature
CC table).
XX
XX SQ Sequence 330 AA;

Query Match 97.5%; Score 1228; DB 9; Length 330;
Best Local Similarity 97.4%; Pred. No. 1.7e-88;
Matches 226; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNKTPRREQYNSTYRVSVLTVLHONMNGKEYCKVSKNKAIPAPIEKT 120
Db 159 NWYVDGVEVHNKTPRREQYNSTYRVSVLTVLHONMNGKEYCKVSKNKAIPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYQQRSLSPGK 232
Db 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYTQKLSLSPGK 330

RESULT 6

AAW26232
ID AAW26232 standard; protein; 232 AA.
XX
XX AC AAW26232;
XX
XX DT 16-MAR-1998 (first entry)
XX
XX DE Human IgG1 hinge/Fc region.
XX
XX KW Fusion protein; hydrophilic spacer; recombinant; expression system;
KW carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.
XX
XX OS Homo sapiens.
XX
XX PN WO9728272-A1.
XX
XX PD 07-AUG-1997.
XX
XX PF 31-JAN-1997; 97WO-US001470.
XX
XX PR 31-JAN-1996; 96US-00595043.
XX
XX PA (TECH-) TECHNOLOGENE INC.
XX
XX PI Sgarlato GD;
XX
XX DR WPI; 1997-402624/37.
XX
XX DR N-PSDB; AAT80158.
XX
XX PT Recombinant protein expression system for fusion protein production -
PT useful for high quantity production of authentic recombinant proteins.
XX
XX PS Example 3; Page 133-134; 194pp; English.
XX
XX CC A novel recombinant vector has been developed which comprises a
CC nucleotide sequence encoding a fusion protein. The fusion protein
CC comprises three domains joined together in order, from N-terminus to C-
CC terminus, of a first domain comprising a protein of interest, a second
CC domain comprising a hydrophilic spacer and an affinity domain, each
CC domain comprising amino acid residues. The present sequence represents
CC the hinge/Fc region of human IgG1, used in example 3 of the present
CC invention. The recombinant vector is used for the production of authentic
CC recombinant proteins of interest. The method of the invention is useful
CC for the expression of fusion proteins capable of isolation by affinity
CC chromatography in pro- or eukaryotic cells. This method allows for the
CC efficient cleavage and generation of authentic proteins of interest that
CC do not contain extraneous (i.e. non-naturally occurring) amino acids
XX
XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.9e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNKTPRREQYNSTYRVSVLTVLHONMNGKEYCKVSKNKAIPAPIEKT 120
Db 61 NWYVDGVEVHNKTPRREQYNSTYRVSVLTVLHONMNGKEYCKVSKNKAIPAPIEKT 120
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYQQRSLSPGK 232
Db 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYTQKLSLSPGK 232

RESULT 7
AAB28690

ID AAB28690 standard; protein; 232 AA.
 XX AC AAB28690;
 XX DT 14-FEB-2001 (first entry)
 XX DE Human IgGgamma1 hinge, CH2 and CH3 regions.
 XX KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
 KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
 KW transplant rejection; cardiovascular disease; arteriosclerosis;
 KW IgGgamma1.
 XX OS Homo sapiens.
 XX PN WO200063253-A1.
 XX PD 26-OCT-2000.
 XX PF 24-MAR-2000; 2000WO-US008004.
 XX PR 16-APR-1999; 99US-00293245.
 XX PA (AMGE-) AMGEN INC.
 XX PI Hsu H, Meng S;
 XX DR WPI; 2000-665240/64.
 XX PT Fusion protein of AGP-1 protein and an Fc region, used to treat
 PT proliferative disorders, immune disorders, and virally-induced disorders.
 XX PS Claim 2; Fig 1; 93pp; English.
 XX CC The present sequence was used in the production of AGP-1 fusion proteins.
 CC AGP-1 is a type II transmembrane protein. The fusion proteins comprise an
 CC Fc immunoglobulin region fused to the N-terminal portion of the AGP-1
 CC protein. The fusion proteins can be used to induce apoptosis in a tissue,
 CC and to treat proliferative disorders, immune disorders, or virally-
 CC induced disorders. The proliferative disorders include cancers, such as
 CC breast, prostate, lung or colon cancer. The viral infections include
 CC hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune
 CC disorders may be autoimmune disorders or transplant rejection.
 CC Cardiovascular diseases such as arteriosclerosis may also be treated. The
 CC AGP-1 containing fusion proteins have increased biological activity
 CC compared to the soluble AGP-1 proteins used in prior art therapies
 XX SQ Sequence 232 AA;
 Query Match 97.2%; Score 1225; DB 3; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYDGVGVHNVKTPREEQNSTYRVSVTLVHQNMMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYDGVGVHNAKTPREEQNSTYRVSVTLVHQNMMNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
 RESULT 8

AAB80897
 ID AAB80897 standard; protein; 232 AA.
 XX AC AAB80897;
 XX DT 31-MAY-2001 (first entry)
 XX DE Human IgGgamma1 hinge, CH2 and CH3 regions.
 XX KW Human; IgGgamma1; anticancer; Antimetastatic; Osteogenic;
 KW lytic bone disease; multiple myeloma; immunoglobulin;
 KW osteoclastic bone metastasis; OPG; osteoprotegerin;
 KW osteoclast formation inhibition; bone resorption inhibition.
 XX OS Homo sapiens.
 XX PN WO200117543-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-US022806.
 XX PR 03-SEP-1999; 99US-00389545.
 XX PA (AMGE-) AMGEN INC.
 XX PI Dunstan CR;
 XX DR WPI; 2001-265936/27.
 XX PT Preventing or treating lytic bone diseases, particularly associated with
 PT cancer or metastasis, by administering an osteoprotegerin polypeptide.
 XX PS Disclosure; Fig 1; 87pp; English.
 XX CC The present invention relates to a method for the prevention or treatment
 CC of lytic bone disease or multiple myeloma. Also the method can be used
 CC for preventing metastasis of cancer to bone or osteosclerotic bone
 CC metastasis. The method comprises administering an OPG (osteoprotegerin)
 CC polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-
 CC AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)
 CC by blocking differentiation from monocytes/macrophage precursors. The
 CC present sequence is the hinge, CH2 and CH3 regions of human IgGgamma1.
 CC This sequence can be used to generate fusion proteins of OPG and
 CC immunoglobulin, for use in the present invention. The generated fusion
 CC proteins can exhibit increased circulating half-lives and slower
 CC clearance times, thereby providing a more sustained activity
 XX SQ Sequence 232 AA;
 Query Match 97.2%; Score 1225; DB 4; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYDGVGVHNVKTPREEQNSTYRVSVTLVHQNMMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYDGVGVHNAKTPREEQNSTYRVSVTLVHQNMMNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
 RESULT 9
 AAY72915

AAE15347 standard; protein; 232 AA.
AAE15347;
09-APR-2002 (first entry)
Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.
Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG;
cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.
Homo sapiens.
WO200181405-A2.
01-NOV-2001.
19-APR-2001; 2001WO-US012836.
21-APR-2000; 2000US-00559001.
(AMGE-) AMGEN INC.
Egrie JC, Elliott SG, Browne JK, Sitney KC;
WPI; 2002-034433/04.
Increasing and maintaining hematocrit in mammal suffering from anemia,
comprising administering hyperglycosylated analog of erythropoietin less
frequently and at lower molar amount of recombinant human erythropoietin.
Example 1; Fig 10; 95pp; English.
The invention relates to a method for increasing and maintaining
haematocrit in a mammal. The method comprises administering a
hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical
composition, less frequently than an equivalent molar amount of and at a
lower molar amount than recombinant human Epo (rHuEpo) to obtain a
comparable target haematocrit. Epo is a glycoprotein hormone necessary
for the maturation of erythroid progenitor cells into erythrocytes. Human
Epo analogue is useful for raising and maintaining haematocrit to a
comparable target haematocrit in a mammal suffering from anaemia
associated with a decline or loss of kidney function, myelosuppressive
therapy comprising chemotherapeutic or anti-viral drugs or associated
with excessive blood loss during surgical procedures, and in cancer
condition. The present sequence is human immunoglobulin G (IgG) gamma 1
constant heavy chain (CH2, CH3) hinge region used to construct Epo
hyperglycosylated analogue fusion protein

AAE15347 standard; protein; 232 AA.
AAE15347;
13-JUN-2001 (first entry)
Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.
Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
periodontal.
Homo sapiens.
WO200118203-A1.
15-MAR-2001.
18-AUG-2000; 2000WO-US022797.
03-SEP-1999; 99US-00389782.
(AMGE-) AMGEN INC.
Dunstan CR, Wooden SK, Mann MB;
WPI; 2001-244572/25.
Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
by e.g. osteoporosis, Paget's disease and osteomyelitis.
Claim 3; Fig 1; 119pp; English.
The patent discloses fusion protein comprising human osteoprotegerin
(OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively
regulates formation of osteoclasts in vitro and in vivo. It blocks the
differentiation of osteoclasts from monocyte or macrophage precursors and
the reabsorption of bone. The OPG-Fc fusion protein is administered for
the treatment of bone loss resulting from osteoporosis, Paget's disease,
osteomyelitis, hypercalcaemia, osteopenia associated with surgery or
steroid administration, osteonecrosis, bone loss due to rheumatoid
arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic
loosening. The present sequence is partial human immunoglobulin G (Ig G)
1 protein comprising the hinge and heavy chain constant regions CH2 and
CH3

AAE15347 standard; protein; 232 AA.
AAE15347;
13-JUN-2001 (first entry)
Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.
Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
periodontal.
Homo sapiens.
WO200118203-A1.
15-MAR-2001.
18-AUG-2000; 2000WO-US022797.
03-SEP-1999; 99US-00389782.
(AMGE-) AMGEN INC.
Dunstan CR, Wooden SK, Mann MB;
WPI; 2001-244572/25.
Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
by e.g. osteoporosis, Paget's disease and osteomyelitis.
Claim 3; Fig 1; 119pp; English.
The patent discloses fusion protein comprising human osteoprotegerin
(OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively
regulates formation of osteoclasts in vitro and in vivo. It blocks the
differentiation of osteoclasts from monocyte or macrophage precursors and
the reabsorption of bone. The OPG-Fc fusion protein is administered for
the treatment of bone loss resulting from osteoporosis, Paget's disease,
osteomyelitis, hypercalcaemia, osteopenia associated with surgery or
steroid administration, osteonecrosis, bone loss due to rheumatoid
arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic
loosening. The present sequence is partial human immunoglobulin G (Ig G)
1 protein comprising the hinge and heavy chain constant regions CH2 and
CH3

QY	121	ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180
Db	121	ISAKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180
QY	181	PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVWHEALHNHYQOQSLSLSPGK	232
Db	181	PVLDSGDSFFLYSKLTVDKSRWQGNVFSQVWHEALHNHYTKQSLSLSPGK	232
RESULT 13			
ADJ57512	ID	ADJ57512 standard; protein; 232 AA.	
XX	AC	ADJ57512;	
XX	XX	06-MAY-2004 (first entry)	
XX	DE	Human IgG1 Fc domain fragment.	
XX	XX	TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;	
KW	KW	cerebroprotective; cytostatic; vasotropic; antirheumatic; antiarthritic;	
KW	KW	antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive;	
KW	KW	hypertensive; cardiac; coagulation Factor VII; human; immunoglobulin G1;	
KW	KW	IgG1.	
OS	OS	Homo sapiens.	
XX	XX	WO2004006962-A2.	
XX	XX	22-JAN-2004.	
XX	XX	09-JUL-2003; 2003WO-DK000481.	
XX	XX	12-JUL-2002; 2002DK-00001099.	
XX	XX	(NOVO) NOVO NORDISK AS.	
XX	PI	Bjorn SE, Nicolaissen EM, Steenstrup TD;	
XX	XX	WPI; 2004-180224/17.	
XX	XX	New compound binding to tissue factor, useful for treating diseases such	
PT	PT	as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.	
XX	PS	Claim 16; SEQ ID NO 7; 61pp; English.	
XX	CC	The invention relates to a compound (I) binding to tissue factor (TF).	
CC	CC	The compound (I) has the formula A-(LM)-C, where A is a FVIIa	
CC	CC	polypeptide, LM is an optional linker group, C comprises an	
CC	CC	immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-	
CC	CC	mediated activated factor VII (FVIIa) activity. (I) is useful as a	
CC	CC	medicament, and for the manufacture of a medicament for preventing or	
CC	CC	treating disease or disorder associated with pathophysiological TF	
CC	CC	activity. The disease or disorder associated with pathophysiological TF	
CC	CC	activity are deep venous thrombosis, arterial thrombosis, post surgical	
CC	CC	thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal	
CC	CC	coronary angioplasty (PTCA), stroke, cancer, tumor metastasis,	
CC	CC	angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis,	
CC	CC	arteriosclerosis and restenosis following angioplasty, acute and chronic	
CC	CC	indications such as inflammation, septic shock, septicemia, hypotension,	
CC	CC	adult respiratory distress syndrome (ARDS), disseminated intravascular	
CC	CC	coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial	
CC	CC	infarction, or prophylactic treatment of mammals with atherosclerotic	
CC	CC	vessels at risk for thrombosis. The present sequence represents the Fc	
CC	CC	domain fragment of human immunoglobulin G1 (IgG1).	
XX	XX	Sequence 232 AA;	
Query Match 97.2%; Score 1225; DB 8; Length 232;			
Best Local Similarity 97.0%; Pred. No. 1.9e-88;			
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;			
QY	1	EPKSCDKHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Db	1	EPKSCDKHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
QY	61	NNYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT	120
Db	61	NNYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT	120
QY	121	ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180
Db	121	ISAKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180
QY	181	PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVWHEALHNHYQOQSLSLSPGK	232
Db	181	PVLDSGDSFFLYSKLTVDKSRWQGNVFSQVWHEALHNHYTKQSLSLSPGK	232
RESULT 14			
ADJ48992	ID	ADJ48992 standard; peptide; 232 AA.	
XX	AC	ADJ48992;	
XX	DT	02-DEC-2004 (first entry)	
XX	DE	Human IgG1 hinge and CH2 region.	
XX	XX	antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;	
KW	KW	anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;	
KW	KW	AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.	
OS	OS	Homo sapiens.	
XX	XX	US2004175824-A1.	
PN	XX	09-SEP-2004.	
XX	XX	21-JAN-2004; 2004US-00761593.	
XX	XX	17-AUG-2001; 2001US-00932812.	
XX	PA	(SUNL/) SUN L K.	
PA	PA	(SUNB/) SUN B N C.	
PA	PA	(SUNC/) SUN C R Y.	
XX	PI	Sun LK, Sun BNC, Sun CRY;	
XX	XX	WPI; 2004-634851/61.	
XX	XX	New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin	
PT	PT	(HuEPO), a peptide linker, and a human IgG Fc variant, is new.	
PT	PT	treating chronic anemia due to renal diseases, cancer chemotherapy, or	
XX	XX	rheumatoid arthritis.	
PS	PS	Disclosure; SEQ ID NO 26; 31pp; English.	
XX	CC	A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin	
CC	CC	(HuEPO), a peptide linker, and a human IgG Fc variant, is new.	
CC	CC	INDEPENDENT CLAIMS are also included for the following: a chinese hamster	
CC	CC	ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in	
CC	CC	its growth medium in excess of 10 µg per million cells in a 24 hour	
CC	CC	period; and a method for making a recombinant fusion protein comprising	
CC	CC	HuEPO, a flexible peptide linker, and a human IgG Fc variant. Preferred	
CC	CC	Protein: The peptide linker containing 20 or fewer amino acids is present	
CC	CC	between HuEPO and the human IgG Fc variant, and comprises two or more	
CC	CC	amino acids selected from glycine, serine, alanine, and threonine. The	
CC	CC	human IgG Fc variant comprises a hinge, CH2, and CH3 domains of human	
CC	CC	IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).	
CC	CC	It also comprises a hinge, CH2, and CH3 domains of human IgG4 with	
CC	CC	Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.	
CC	CC	20). It further comprises a hinge, CH2, and CH3 domains of human IgB1	
CC	CC	with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino	
CC	CC	acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro	
CC	CC	biological activity similar to or higher than that of rHuEPO on a molar	

CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line
CC producing the HuEPO-L-vFc fusion protein in its growth medium in excess
CC of 30 μ mol/l per million cells in a 24 hour period. The human IgG Fc
CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from
CC IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
CC the IgG Fc contains amino acid mutations to attenuate effector functions,
CC a flexible peptide linker containing 20 or fewer amino acids is present
CC between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion
CC protein exhibits in vitro biological activity similar to or higher than
CC that of HuEPO on a molar basis. Preferred Method: Making a recombinant
CC fusion protein comprising HuEPO, a flexible peptide linker, and a human
CC IgG Fc variant comprises: generating a CHO-derived cell line; growing the
CC cell line where the recombinant protein is expressed in its growth medium
CC in excess of 10 μ mol/l per million cells in a 24 hour period; and
CC purifying the expressed protein from (b), where the recombinant fusion
CC protein exhibits in vitro biological activity similar to or higher than
CC that of HuEPO on a molar basis. Antianemic; Nephrotropic. No biological
CC data given. None given. Administration can be through subcutaneous or
CC intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion
CC protein is useful for treating patients with chronic anemia due to renal
CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for
CC HIV infection, or myelodysplastic syndrome. It is also useful in the
CC treatment of renal failure. A fusion protein was assembled from several
CC DNA segments. To obtain the gene encoding the leader peptide and mature
CC protein of human erythropoietin (EPO), cDNA library of human fetal liver
CC or kidney was used as the template in polymerase chain reaction (PCR).
CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a
CC restriction enzyme cleavage site is used as the 5' oligonucleotide
CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon
CC and incorporates a BamHI site. The resulting DNA fragments of
CC approximately 600 bp were inserted into a holding vector such as pUC19 at
CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the
CC human EPO gene was confirmed by DNA sequencing.

XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.9e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLTQHNMMNGEKYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLTQHNMMNGEKYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVPCFSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 15

ADU51146

ID ADU51146 standard; protein; 232 AA.

XX AC ADU51146;

XX XX 27-JAN-2005 (first entry)

XX DE Human spleen-expressed receptor-related solubility-promoting protein.

XX KW immunosuppressive; cytostatic; antiinflammatory; immune modulation;
KW intercellular communication; autoimmune disease; cancer; neoplasm;
KW transplant rejection; immune disorder; inflammation; gene therapy.

OS Homo sapiens.

XX

PN WO2004096976-A2.
XX 11-NOV-2004.
XX 29-APR-2004; 2004WO-EP0004562.
XX 30-APR-2003; 2003US-0467206P.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS PHARMA GMBH.
XX (SCRI) SCRIPPS RES INST.
XX Kaye J, Wilkinson B;
XX WPI; 2004-804740/79.
XX New purified spleen expressed (SPEX) polypeptide useful for modulating
XX lymphocyte activation and the immune response in disorders including
XX autoimmunity, cancer, transplant rejection and inflammation.
XX Disclosure; SEQ ID NO 97; 98pp; English.
XX The invention relates to a novel purified polypeptide comprising any of
XX SEQ ID Nos: 3, 7, 9, 11, 45 or 88, or an amino acid sequence that is 95%
XX or more identical to the amino acid sequences and which includes an
XX immunoglobulin like domain structure. The polypeptide of the invention
XX demonstrates immunosuppressive, cytostatic and antiinflammatory
XX activities and is a spleen-expressed (SPEX) polypeptide. The methods and
XX compositions of the present invention may be useful for modulating
XX lymphocyte activation and the immune response in a variety of conditions
XX including autoimmunity, cancer, transplant rejection and inflammation.
XX Such modulation may be achieved via the use of gene therapy. The current
XX sequence is that of the human spleen-expressed (SPEX) receptor-related
XX solubility-promoting protein of the invention.

XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.9e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLTQHNMMNGEKYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLTQHNMMNGEKYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVPCFSCVMHEALHNHYQOQSLSLSPGK 232

Search completed: November 30, 2005, 00:51:22

Job time : 113.536 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:46:45 ; Search time 21.8551 Seconds
(without alignments)
1021.378 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPCPAPELL.....MHEALHNHYQQRSLSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	330	1 GHU	Ig gamma-1 chain C
2	1219	96.7	374	2 S69339	Ig heavy chain V r
3	1217	96.6	255	4 S31866	Ig gamma-1 chain C
4	1172	93.0	234	2 P70207	Ig gamma chain C r
5	1138	90.3	377	2 A23511	Ig gamma-3 chain C
6	1136	90.2	377	2 A60764	Ig gamma-3 chain C
7	1123	89.1	289	1 G3HUWI	Ig gamma-3 heavy c
8	1107	87.9	326	1 G2HU	Ig gamma-2 chain C
9	1097	87.1	327	1 G4HU	Ig gamma-4 chain C
10	883	70.1	323	1 GHRB	Ig gamma chain C r
11	868.5	68.9	328	2 I47160	Ig gamma 2b chain
12	868.5	68.9	328	2 I47159	Ig gamma 2a chain
13	865	68.7	277	2 I47162	Ig gamma 4 chain c
14	858	68.1	329	1 G2GP	Ig gamma-2 chain C
15	847.5	67.3	328	2 I47158	Ig gamma 1 chain c
16	840.5	66.7	328	2 I47161	Ig gamma 3 chain c
17	820	65.1	470	2 S22080	Ig heavy chain pre
18	813	64.5	333	2 PS0018	Ig gamma-2b chain
19	812.5	64.5	328	1 G3MSC	Ig gamma-3 chain C
20	811.5	64.4	309	2 C30554	Ig heavy chain C r
21	811.5	64.4	472	2 S31459	Ig gamma-1 chain -
22	801.5	63.6	398	1 G3MSM	Ig gamma-3 chain C
23	794.5	63.1	444	2 PC4436	monoclonal antibody
24	789.5	62.7	324	1 G1MS	Ig gamma-1 chain C
25	784.5	62.3	326	2 PS0017	Ig gamma-1 chain C
26	784.5	62.3	393	1 G1MSM	Ig gamma-1 chain C
27	776.5	61.6	329	2 S00847	Ig gamma-2c chain
28	776	61.6	330	1 G2MSA	Ig gamma-2a chain
29	776	61.6	469	2 S37483	Ig gamma-2a chain

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: UNIPARC:UPI0000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Cross-references: UNIPARC:UPI0000017378D

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A:Cross-references: UNIPARC:UPI000017378E

A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2b chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2b chain C
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma heavy cha
Ig heavy chain VHI
Ig heavy chain V-I
Ig gamma-1 chain C
Ig Y heavy chain (pre
Ig mu chain C regi
Ig mu chain C regi

30 772 61.3 335 1 G2MSAB
31 771 61.2 399 1 G2MSAM
32 761 60.4 446 2 S40295
33 751.5 59.6 474 1 G2MS11
34 747.5 59.3 322 2 PS0019
35 746.5 59.2 405 1 G2MSBM
36 735 58.3 327 2 S06611
37 731.5 58.1 475 2 S01321
38 669 53.1 180 2 S69340
39 549 43.6 249 2 S69340
40 547 43.4 218 2 A36040
41 542 43.0 152 2 S14236
42 366.5 29.1 572 2 B46529
43 357 28.3 549 2 S04945
44 353 28.0 343 2 S25644
45 353 28.0 455 1 MHMS

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Cross-references: UNIPARC:UPI000017378F
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1993
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Cross-references: UNIPARC:UPI0000173790
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 97.2%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 1.7e-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSGVSFFLYSKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 232
Db 279 PVLDSGVSFFLYSKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
RESULT 2
S69339
Ig heavy chain v region precursor - human
C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khanlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khanlich, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
Query Match 96.7%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 5.5e-85;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 143 EPKSCDKTHCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 120
Db 203 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 262
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 263 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 322
QY 181 PVLDSGVSFFLYSKLTVDKSRQOGNVFSCSVNHEALHNHYQORSLSLSPGK 232
Db 323 PVLDSGVSFFLYSKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 374
RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
Query Match 96.6%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 4.9e-85;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 EPKSCDKTHCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 24 EPKSCDKTHCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 120
Db 84 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 143


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Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 144 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 203
|||||
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
|||||
Db 204 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 255
|||||

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R: Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
A:Cross-references: UNIPARC:UPI0000176F05
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 1172; DB 2; Length 234;
Best Local Similarity 95.6%; Pred. No. 1.1e-81;
Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
|||||
Db 10 EPKSCDTTHTCPPCAAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 69
|||||
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 120
|||||
Db 70 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 129
|||||
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 130 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 189
|||||
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQS 225
|||||
Db 190 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKS 234
|||||

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R: Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:G33070; PIDN:CAA272
C:Genes: IGHG3
A:Map position: 14q32.33-14q32.33
A:Map position: 14q32.33-14q32.33
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 1138; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 7.5e-79;

Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 144 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 203
|||||
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 120
|||||
Db 206 KWIYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 265
|||||

RESULT 7
G3HUW1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
A:Accession: A90442; A92219; A90198; A93915; A02149
R: Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein
A:Reference number: A90442; MUID:81021548; PMID:6774747
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
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Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
|||||
Db 146 EPKSCDTPPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 205
|||||
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 120
|||||
Db 206 KWIYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 265
|||||
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 266 ISKTKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 325
|||||
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
|||||
Db 326 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 377
|||||

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C:Accession: A60764
R: Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8MAY9; UNIPARC:UPI00000176F0B
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 1136; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 1.1e-78;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
|||||
Db 146 EPKSCDTPPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 205
|||||
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 120
|||||
Db 206 KWIYVDGVEVHNKTKPREEQNSTYRVSVLTVHLQONMNGKEYKKCKVSNKALPAPIEKT 265
|||||
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
|||||
Db 266 ISKTKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 325
|||||
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
|||||
Db 326 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 377
|||||

RESULT 7
G3HUW1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
A:Accession: A90442; A92219; A90198; A93915; A02149
R: Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein
A:Reference number: A90442; MUID:81021548; PMID:6774747
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
```


QY 45 TCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYNSTRYRVSVLTLVHLQNMWNGKEY 104
Db 136 TCVVVDVSDPDPEVKFQVWYINNEQVRRFARPLDRLRQFNSTRYRVSFLPIHQDMLRGKGF 195
QY 105 KCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAV 164
Db 196 KCKVHNKALPAPIEKTISKARGQLPKVYTMGPPEELSSRSVSLTCMINGFYPSDISV 255
QY 165 EWSNGOPENNYKTTTPVLDVSGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQQR 224
Db 256 EWEKNGKAEDNYKTTTPVLDVSGSFYLYNKLSVPTSEWQGRDFTCSVMHEALHNHYTK 315
QY 225 SLSLSPGK 232
Db 316 SISRSPOGK 323

RESULT 11
I47160
Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47160
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47160
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PFI
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 1.6e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

QY 11 CPPCPAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
Db 106 CPICPACE -SPGPSVFIFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164
QY 71 NVKTKPREEQYNSTRYRVSVLTLVHLQNMWNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKERQFNSTRYRVSFLPIHQDMLRGKGFCKVNNKDLPAPITRIISKAKGQTR 224

RESULT 12
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>

A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PFI
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 1.6e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

QY 11 CPPCPAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
Db 106 CPICPACE -SPGPSVFIFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164
QY 71 NVKTKPREEQYNSTRYRVSVLTLVHLQNMWNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKERQFNSTRYRVSFLPIHQDMLRGKGFCKVNNKDLPAPITRIISKAKGQTR 224

QY 131 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVESNGQ--PENNYKTTTPVLDVSGS 188
Db 225 POVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPQDQVDGT 284

QY 189 FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGK 232
Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTKSISKTPGK 328

RESULT 13
I47162
Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47162
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
A;Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PFI
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 865; DB 2; Length 277;
Best Local Similarity 69.0%; Pred. No. 2.5e-58;
Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;

QY 8 THTCPCEP-APELLG-SPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65
Db 49 TKTTPCPICPACGPGPSAFIFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 108

QY 66 GVEVHNKTKPREEQYNSTRYRVSVLTLVHLQNMWNGKEYKCKVSNKALPAPIEKTISKAK 125
Db 109 GVEVHTAQRPKERQFNSTRYRVSFLPIHQDMLRGKGFCKVNNKDLPAPITRIISKAK 168

QY 126 VQPREPVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVESNGQ--PENNYKTTTPVLD 183
Db 169 GQTRERQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPQ 228

QY 184 DSVGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGK 232
Db 229 DVDGTGYFLYSKLAVDKASWQGRDFTQCAVMHEALHNHYTKSISKTPGK 277

RESULT 14
G2GP
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004

C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI0000017379E
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
A;Cross-references: UNIPARC:UPI0000017379F
R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
A;Reference number: A90359; MUID:71058486; PMID:5538616
A;Accession: A90359
A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI000001737A0; UNIPARC:UPI000001737A1
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
A;Cross-references: UNIPARC:UPI000001737A2
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
A;Molecule type: protein
A;Residues: 227-311 <TR2>
A;Cross-references: UNIPARC:UPI000001737A3
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:248-308/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent)
F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No.1e-57; Mismatches 42; Indels 6; Gaps 2;
Matches 157; Conservative 28;

Qy 1 EPKSCDKTHTPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 101 ZFBPC-----TCPKCPPEPENGSPSVFIFPPKPKDTLMISLTPRVTCTVVVDVSDQPEVQF 156

Qy 61 NNYVDGVEVHVKTPREYQNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 157 TWFVDNKPVGNAETKPRVQYNTTFRVESVLPFQHDWLGRGKFKCKVYNKALPAPIEKT 216

Qy 121 ISKAKVQPREQYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAEVESNGQP--ENNYKT 178

Db 217 ISKTGAPRMPDVYTLPPSRDELSKGVSVTCLIIINFFPADIHVEWASNRVPVSEKEYKN 276
Qy 179 TTPVLDVSGSFYLYSKLTVDDKSRWQGNVFCSCVMHEALHNHYQORSLSPG 231
Db 277 TPPIEDAGSYFLYSLKLVDDKSAWDGTVYTCVMHEALHNHYTQKAISRSPG 329

RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI00000115523; EMBL:U03778; NID:9433121; PIDN:AA52216.1; P1
C;Genetics:
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
Query Match 67.3%; Score 847.5; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 6.4e-57;
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

Qy 10 TCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 69
Db 105 TCPICPGCE-VAGSPSVFIFPPKPKDTLMISQTPVTCVVVDVSKHAELVQFSWYVDGVEV 163
Qy 70 HNVKTKPREQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPR 129
Db 164 HTAETRPKEQFNSTYRVSVLPFQHDWLKGEKFKCKVNNVDLPAPITRTISKAGQSR 223
Qy 130 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAEVESNGQ--PENNYKTTTPPVLDVSG 187
Db 224 EPQVYTLPPPAEELSRKSVTLTCLVIGFYPPDIHVEWKSNGQPEPTRTTPPQDDVDG 283
Qy 188 SFELYSLKTVDDKSRWQGNVFCSCVMHEALHNHYQORSLSPG 232
Db 284 TFFLYSLKLVADKARDHGDGKFECAVMHEALHNHYTQKSISKTQCK 328

Search completed: November 30, 2005, 01:11:21
Job time : 22.8551 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:43:39 ; Search time 127.768 Seconds
(without alignments)
1281.091 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

Sequence: 1 EPRKCDTHTCCPCPAPELL.....MHEALHNYQORSLSLSPGX 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 IGHG1_HUMAN	P01857 homo sapien
2	1225	97.2	465	2 Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	1225	97.2	466	2 Q6IN78_HUMAN	Q6in78 homo sapien
4	1225	97.2	469	2 Q569F4_HUMAN	Q569f4 homo sapien
5	1225	97.2	469	2 Q7Z7P5_HUMAN	Q7z7p5 homo sapien
6	1225	97.2	470	2 Q7Z5W1_HUMAN	Q7z5w1 homo sapien
7	1225	97.2	470	2 Q6PJA4_HUMAN	Q6pja4 homo sapien
8	1225	97.2	472	2 Q6N089_HUMAN	Q6n089 homo sapien
9	1225	97.2	475	2 Q5EFES_HUMAN	Q5efes homo sapien
10	1225	97.2	475	2 Q6GMW7_HUMAN	Q6gmw7 homo sapien
11	1225	97.2	476	2 Q6GMX1_HUMAN	Q6gmx1 homo sapien
12	1225	97.2	679	2 Q96PQ8_HUMAN	Q96pq8 homo sapien
13	1221	96.9	473	2 Q6P055_HUMAN	Q6p055 homo sapien
14	1221	96.9	475	2 Q6MZQ6_HUMAN	Q6mzq6 homo sapien
15	1221	96.9	480	2 Q6N094_HUMAN	Q6n094 homo sapien
16	1221	96.9	481	2 Q6N097_HUMAN	Q6n097 homo sapien
17	1221	96.9	482	2 Q7Z351_HUMAN	Q7z351 homo sapien
18	1219	96.7	348	2 Q6PYX1_HUMAN	Q6pyx1 homo sapien
19	1219	96.7	473	2 Q6MZV7_HUMAN	Q6mzv7 homo sapien
20	1219	96.7	478	2 Q6P181_HUMAN	Q6p181 homo sapien
21	1219	96.7	480	2 Q6PJF1_HUMAN	Q6pjf1 homo sapien
22	1218	96.7	466	2 Q6N096_HUMAN	Q6n096 homo sapien
23	1214	96.3	475	2 Q6N095_HUMAN	Q6n095 homo sapien
24	1214	96.3	544	2 Q6P195_HUMAN	Q6p195 homo sapien
25	1196	94.9	487	2 Q55ZL2_MOUSE	Q55z12 mus sp. fr/
26	1164	92.4	475	2 Q5RE17_PONPY	Q5re17 pongo pygma
27	1138	90.3	354	2 Q86TT2_HUMAN	Q86tt2 homo sapien
28	1138	90.3	518	2 Q6N030_HUMAN	Q6n030 homo sapien
29	1138	90.3	519	2 Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	1134	90.0	521	2 Q8N4Y9_HUMAN	Q8n4y9 homo sapien
31	1128	89.5	290	1 IGHG3_HUMAN	P01860 homo sapien

32 1123 89.1 509 2 Q8NF17_HUMAN Q8nf17 homo sapien
33 1107 87.9 326 1 IGHG2_HUMAN IGhg2_HUMAN
34 1107 87.9 417 2 Q6N093_HUMAN Q6n093 homo sapien
35 1104 87.6 464 2 Q6MZU6_HUMAN Q6mzu6 homo sapien
36 1102 87.5 465 2 Q6P6C4_HUMAN Q6p6c4 homo sapien
37 1097 87.1 327 1 IGHG4_HUMAN P01861 homo sapien
38 1097 87.1 473 2 Q8TC63_HUMAN Q8tc63 homo sapien
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40 1088 86.3 476 2 Q6MZK7_HUMAN Q6mzk7 homo sapien
41 883 70.1 323 1 GC_RABIT P01870 oryctolagus
42 877.5 69.6 337 2 Q95M34_HORSE Q95m34 equus caball
43 858 68.1 329 1 IGHG2_CAVPO P01862 cavia porce
44 813 64.5 333 1 GCB_RAT P20761 rattus norv
45 813 64.5 469 2 Q5M839_RAT Q5m839 rattus norv

ALIGNMENTS

RESULT 1
IGHG1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP PROTEIN SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
RN [5]
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.

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RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC GIM(3) marker and the GIM (non-1) markers.
CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
DR PIR; A93433; GHU.
DR PDB; 1AJ7; X-ray; H=1-103.
DR PDB; 1AOK; X-ray; H=1-103.
DR PDB; 1DSB; X-ray; B/H=1-101.
DR PDB; 1DSI; X-ray; H=1-101.
DR PDB; 1DVV; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1HZH; X-ray; H/K=1-330.
DR PDB; 1I72; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1LOQ; X-ray; A/B=119-330.
DR PDB; 1T83; X-ray; A/B=107-330.
DR PDB; 2RCS; X-ray; H=1-103.
DR HGNC; HGNC:5525; IGHG1.
DR MTM; 147100; ...
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR PROSITE; PSS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
RN REGION 1 98 CH1.

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FT REGION 99 110 Hinge.
FT REGION 111 223 CH2.
FT REGION 224 330 CH3.
FT CARBOHYD 180 180 N-linked (GlcNAc...),
FT DISULFID 27 83 Interchain (with light chain).
FT DISULFID 103 103 Interchain (with heavy chain).
FT DISULFID 109 109 Interchain (with heavy chain).
FT DISULFID 112 112 Interchain (with heavy chain).
FT DISULFID 144 204 Interchain (with heavy chain).
FT DISULFID 250 308 Interchain (with heavy chain).
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FT 239 D -> E (in GIM(non-1) marker).
FT /FTId=VAR_003887.
FT 241 L -> M (in GIM(non-1) marker).
FT /FTId=VAR_003888.
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FT STRAND 23 24
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FT TURN 136 137
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FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

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Query Match 97.2%; Score 1225; DB 1; Length 330;
 Best Local Similarity 97.0%; Pred. No. 5.9e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60


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Db 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
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Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQNMMNGKEYCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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Query Match 97.2%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 9.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 234 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 294 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQNMMNGKEYCKVSNKALPAPIEKT 353
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 354 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 413
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 414 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 465

RESULT 3
Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSP; P01861; 1A0Q.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; C1-set; 3.
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DR SMART; SM00409; IG: 2;
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0CBCEB81076E CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 466;
Best Local Similarity 97.0%; Pred. No. 9.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHCPCPAPELLGGPSVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDDEVKF 60
DB 235 EPKSCDKHTHCPCPAPELLGGPSVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDDEVKF 294
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQNWMNGKEYCKVSNKALPAPIEKT 120
DB 295 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQNWMNGKEYCKVSNKALPAPIEKT 354
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
DB 355 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 414
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 232
DB 415 PVLDSGDSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 466

RESULT 4
Q569F4_HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448B3047784F CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 466;
Best Local Similarity 97.0%; Pred. No. 9.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHCPCPAPELLGGPSVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDDEVKF 60
DB 235 EPKSCDKHTHCPCPAPELLGGPSVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDDEVKF 294
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQNWMNGKEYCKVSNKALPAPIEKT 120
DB 295 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQNWMNGKEYCKVSNKALPAPIEKT 354
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
DB 355 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 414
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 232
DB 415 PVLDSGDSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 466

RESULT 4
Q569F4_HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448B3047784F CRC64;
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DR SMART: SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5B812BAAF795C CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 469;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 238 EPKSCDKTHTCCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297
QY 61 NWYDGVGVHNVKTPREEQNSTYRVVSVLTCLVKGFPSPDIQVWESNGQPPENNYKTP 120
DB 298 NWYDGVGVHNAKTPREEQNSTYRVVSVLTCLVKGFPSPDIQVWESNGQPPENNYKTP 357
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPPENNYKTP 180
DB 358 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPPENNYKTP 417
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
DB 418 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQOQSLSLSPGK 469

RESULT 6
Q725W1 HUMAN
ID Q725W1_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Young A.C., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; I9_C1.
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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCCPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 61 NWYDGVGVHNVKTPREEQNSTYRVVSVLTCLVKGFPSPDIQVWESNGQPPENNYKTP 120
DB 299 NWYDGVGVHNAKTPREEQNSTYRVVSVLTCLVKGFPSPDIQVWESNGQPPENNYKTP 358
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPPENNYKTP 180
DB 359 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPPENNYKTP 418
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
DB 419 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQOQSLSLSPGK 470

RESULT 7
Q6PJ4 HUMAN
ID Q6PJ4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJ4.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IG_H1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Young A.C., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMK; Q6PUA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 470 AA; 51716 MW; 7849556A11FD7D99 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
DB 299 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 358
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 418
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYQORSLSLSPGK 232
DB 419 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYTQKLSLSPGK 470

RESULT 8
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686p15220.
GN Name=DKF2p686p15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CA845781.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

us-09-847-208b-3.rup

Query Match 97.2%; Score 1225; DB 2; Length 472;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 241 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 300
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
DB 301 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 360
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 361 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 420
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYQORSLSLSPGK 232
DB 421 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYTQKLSLSPGK 472

RESULT 9
QSEF5 HUMAN
ID QSEF5 HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEF5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal antibody T125."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AAM82028.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL. 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy chain.
FT SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

us-09-847-208b-3.rup

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
DB 304 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 363
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
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Db 364 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 423
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOBSLSLSPOK 232
Db 424 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOBSLSLSPOK 475

RESULT 10
Q6GMW7 HUMAN PRELIMINARY; PRT; 475 AA.
ID Q6GMW7 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madsen A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; Pf07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS08335; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTCPCPAPPELLGGPSVFLPPLPKDKTLMTISRTPEVTCVVVDVSHEDPEVKF 60
Db 244 EPKSCDKHTCPCPAPPELLGGPSVFLPPLPKDKTLMTISRTPEVTCVVVDVSHEDPEVKF 303
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Best Local Similarity 97.0%; Pred. No. 9.3e-90;			
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;			
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Db	245	EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	304
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Db	305	NWYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT	364
QY	121	ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP	180
Db	365	ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP	424
QY	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK	232
Db	425	PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	476
RESULT 12			
Q96PQ8 HUMAN			
ID	Q96PQ8	HUMAN PRELIMINARY; PRT; 679 AA.	
AC	Q96PQ8;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Factor VII active site mutant immunoconjugate.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;		
RA	Hu Z., Garen A.;		
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor		
RT	cells for immunotherapy in mouse models of prostatic cancer.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Hu Z., Garen A.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF272774; AAKS8686.2; -, mRNA.		
DR	HSSP; P08709; IKLI.		
DR	SMR; Q96PQ8; 39-180, 191-444, 447-679.		
DR	Ensembl; ENSG00000057593; Homo sapiens.		
DR	GO; GO:0005576; C:extracellular region; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO; GO:0004295; F:trypsin activity; IEA.		
DR	InterPro; IPRO00152; Asx hydroxyl_S.		
DR	InterPro; IPRO00742; EGF^2.		
DR	InterPro; IPRO01881; EGF^Ca.		
DR	InterPro; IPRO01438; EGF^II.		
DR	InterPro; IPRO06209; EGF^like.		
DR	InterPro; IPRO02383; GLA^blood.		
DR	InterPro; IPRO07110; Ig-like.		
DR	InterPro; IPRO03597; Ig-cl.		
DR	InterPro; IPRO03006; Ig_MHC.		
DR	InterPro; IPRO01314; Peptidase_S1A.		
DR	InterPro; IPRO01254; Peptidase_S1_S6.		
DR	Pfam; PF07654; C1-set; 2.		
DR	Pfam; PF00008; EGF; 1.		
DR	Pfam; PF00594; Gla; 1.		
DR	Pfam; PF00089; Trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	PRINTS; PR00010; EGF^BLOOD.		
DR	PRINTS; PR00001; GLABLOOD.		
DR	SMART; SM00179; EGF_CA; 1.		

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.;
RC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC065820; AAH5820.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 473;
Best Local Similarity 96.6%; Pred. No. 1.9e-89;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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DB 242 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 302 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 361

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
DB 362 ISKAKGQPREFOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 421

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 422 PVLDSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEGLHNHYTKQSLSLSPGK 473

RESULT 14
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ID Q6MZ06_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZ06_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G1190.
GN Name=DKFZp686G1190;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAB5972.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D33AEC18 CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 480;
Best Local Similarity 96.6%; Pred. No. 2e-89;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 242 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301

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DB 302 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 361

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
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QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 422 PVLDSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEGLHNHYTKQSLSLSPGK 473

RESULT 15
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ID Q6N094_HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686O01196.
GN Name=DKFZp686O01196;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAB45776.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D33AEC18 CRC64;

Query Match 96.9%; Score 1221; DB 2; Length 480;
Best Local Similarity 96.6%; Pred. No. 2e-89;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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Db	369	ISKAKQPREPQVYTLPPSRDELTKNOVSLTCLV	KGFYPSDIAVEWESNGQPENNYK	428
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:51:35 ; Search time 27.7391 Seconds
(without alignments)
691.469 Million cell updates/sec

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Perfect score: 1260
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Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	232	1	US-08-595-043A-50
2	1225	97.2	232	2	US-09-968-362A-26
3	1225	97.2	232	2	US-09-932-812A-26
4	1225	97.2	331	2	US-09-178-869-2
5	1225	97.2	331	2	US-09-761-413-2
6	1225	97.2	360	2	US-09-180-100-11
7	1225	97.2	360	2	US-09-949-713-11
8	1225	97.2	371	1	US-08-236-311-7
9	1225	97.2	371	2	US-08-457-918-7
10	1225	97.2	371	2	US-10-157-408-7
11	1225	97.2	376	2	US-09-180-100-22
12	1225	97.2	376	2	US-09-949-713-22
13	1225	97.2	379	2	US-10-679-999-9
14	1225	97.2	396	1	US-08-784-512-3
15	1225	97.2	396	2	US-09-176-228-3
16	1225	97.2	424	4	PCT-US95-03866-12
17	1225	97.2	424	4	PCT-US95-03866-14
18	1225	97.2	437	4	PCT-US96-10043-11
19	1225	97.2	442	4	US-08-472-888A-7
20	1225	97.2	442	4	PCT-US96-10043-9
21	1225	97.2	446	2	US-08-397-411-7
22	1225	97.2	449	1	US-08-458-516-13
23	1225	97.2	452	2	US-09-773-877B-16
24	1225	97.2	459	1	US-08-157-101A-7
25	1225	97.2	462	2	US-09-773-877B-18
26	1225	97.2	467	2	US-08-030-175-41
27	1225	97.2	467	2	US-08-030-175-42

28	1225	97.2	470	2	US-10-104-047-3730	Sequence 3730, Appl
29	1225	97.2	475	2	US-09-740-002-27	Sequence 27, Appl
30	1225	97.2	476	1	US-08-378-939-10	Sequence 10, Appl
31	1225	97.2	476	2	US-08-487-550-4	Sequence 4, Appl
32	1225	97.2	476	2	US-08-487-550-12	Sequence 12, Appl
33	1225	97.2	476	2	US-09-526-098-4	Sequence 4, Appl
34	1225	97.2	476	2	US-09-526-098-12	Sequence 12, Appl
35	1225	97.2	476	2	US-09-383-916-4	Sequence 4, Appl
36	1225	97.2	476	2	US-09-383-916-12	Sequence 12, Appl
37	1225	97.2	476	2	US-09-758-173-4	Sequence 4, Appl
38	1225	97.2	476	2	US-09-758-173-12	Sequence 12, Appl
39	1225	97.2	476	2	US-09-576-424-4	Sequence 4, Appl
40	1225	97.2	476	2	US-09-576-424-12	Sequence 12, Appl
41	1225	97.2	478	2	US-08-487-550-8	Sequence 8, Appl
42	1225	97.2	478	2	US-09-526-098-8	Sequence 8, Appl
43	1225	97.2	478	2	US-09-383-916-8	Sequence 8, Appl
44	1225	97.2	478	2	US-09-758-173-8	Sequence 8, Appl
45	1225	97.2	478	2	US-09-576-424-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-043A-50

Query Match	97.2%	Score 1225;	DB 1;	Length 232;
Best Local Similarity	97.0%;	Pred. No. 3.5e-116;		
Matches 225;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
Db	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
Qy	61	NWYDGVGVHNVKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT	120	
Db	61	NWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT	120	

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QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 232
DB 181 PVLDSGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 232

RESULT 2
US-09-968-362A-26
; Sequence 26, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-26

Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTCCPPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 232
DB 181 PVLDSGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 232

RESULT 3
US-09-932-812A-26
; Sequence 26, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-932-812A-26
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Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTCCPPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 232
DB 181 PVLDSGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 232

RESULT 4
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hamman, Joseph P
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 100 EPKSCDKHTCCPPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 160 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 219
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 220 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 279
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 232
DB 280 PVLDSGSFPLYSKLTVDKSRWQOQGNVFSCSVMHQALHNNHYQKSLSPGK 331

RESULT 5
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
```

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; APPLICANT: Hamman, Joseph P.
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/761,413
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/178,869
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-761-413-2

Query Match          97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 100 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 159
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
Db 160 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 219
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 220 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 279
Qy 181 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 280 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 331

RESULT 6
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-180-100-11

Query Match          97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 129 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 188
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
Db 189 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 248
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 249 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 308
Qy 181 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 309 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 360

RESULT 7
US-09-949-713-11
; Sequence 11, Application US/09949713
; Patent No. 6953847
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6953847io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-949-713-11

Query Match          97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 129 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 188
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
Db 189 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 248
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 249 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 308
Qy 181 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 309 PVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 360

RESULT 8
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311

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; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-236-311-7

Query Match          97.2%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 140 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
QY 61 NNYVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 200 NNYVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 319
QY 181 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCFSCVMHEALHNNHYTKQSLSPGK 232
DB 320 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCFSCVMHEALHNNHYTKQSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918

; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-236-311-7

Query Match          97.2%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 140 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
QY 61 NNYVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 200 NNYVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 319
QY 181 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCFSCVMHEALHNNHYTKQSLSPGK 232
DB 320 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCFSCVMHEALHNNHYTKQSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918

; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-457-918-7

Query Match          97.2%; Score 1225; DB 2; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 140 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
QY 61 NNYVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 200 NNYVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 319
QY 181 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCFSCVMHEALHNNHYTKQSLSPGK 232
DB 320 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCFSCVMHEALHNNHYTKQSLSPGK 371

RESULT 10
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```


APPLICANT: Mann, Michael B.
APPLICANT: Hecht, Randy I.
TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/679,999
FILING DATE: 06-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/568,528
FILING DATE: 09-May-2000
APPLICATION NUMBER: 09/267,517
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W.
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: A-416
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1
OTHER INFORMATION: /note= "Met (ATG) starts at -1"
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-679-999-9

Query Match 97.2%; Score 1225; DB 2; Length 379;
Best Local Similarity 97.0%; Pred. No. 7.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 2 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 61
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
Db 62 NWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 121
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLIVKGFPYSDIAVESNGQPENNYKTTTP 180
Db 122 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLIVKGFPYSDIAVESNGQPENNYKTTTP 181
QY 181 PVLDVSGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
Db 182 PVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 233

RESULT 14
US-08-784-512-3
Sequence 3, Application US/08784512
Patent No. 5872209
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENMUELLER, Bernd
APPLICANT: BUETTNER, Frank

APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGS 1)
TITLE OF INVENTION: and native aggregan to study the proteolytic activity of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396
US-08-784-512-3

Query Match 97.2%; Score 1225; DB 1; Length 396;
Best Local Similarity 97.0%; Pred. No. 7.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 165 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 224
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
Db 225 NWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 284
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLIVKGFPYSDIAVESNGQPENNYKTTTP 180
Db 285 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLIVKGFPYSDIAVESNGQPENNYKTTTP 344
QY 181 PVLDVSGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
Db 345 PVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 396

RESULT 15
US-09-176-228-3
Sequence 3, Application US/09176228
Patent No. 6180334
GENERAL INFORMATION:
APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENMUELLER, Bernd
APPLICANT: BUETTNER, Frank
APPLICANT: CATERSON, Bruce

;; APPLICANT: HUGHES, Clare
;; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
;; TITLE OF INVENTION: and native aggregan to study the proteolytic activity of
;; TITLE OF INVENTION: "Aggrecanase" in cell culture systems
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: Suite 500, 3000 K Street, N.W.
;; CITY: Washington, D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/176,228
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/784,512
;; FILING DATE: 17-JAN-1997
;; APPLICATION NUMBER: EP 96100682.2
;; FILING DATE: 18-JAN-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GRANADOS, Patricia D.
;; REGISTRATION NUMBER: 33,683
;; REFERENCE/DOCKET NUMBER: 18748/311
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 396 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..396
US-09-176-228-3

Query Match 97.2%; Score 1225; DB 2; Length 396;
Best Local Similarity 97.0%; Pred. No. 7.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 165 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLTQHONMNGKEYKKCKVSNKALPAPIEKT 120
Db 225 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLTQHONMNGKEYKKCKVSNKALPAPIEKT 284
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 285 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 344
Qy 181 PVLDVSGSFYLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQORSLSPGK 232
Db 345 PVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQORSLSPGK 396

Search completed: November 30, 2005, 01:12:51
Job time : 28.7391 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:56:45 ; Search time 97.087 Seconds
(without alignments)
998.449 Million cell updates/sec

Title: US-09-847-208B-3
Perfect score: 1260
Sequence: 1 EPKSCDKHTCCPCPAPELL.....MHEALHNHYQQRSLSPGK 232

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260	100.0	232	3	US-09-847-208-3
2	1260	100.0	232	4	US-10-000-439-3
3	1260	100.0	330	3	US-09-847-208-2
4	1260	100.0	330	4	US-10-000-439-2
5	1260	100.0	569	3	US-09-847-208-7
6	1260	100.0	569	4	US-10-000-439-7
7	1228	97.5	330	5	US-10-966-673-29
8	1225	97.2	232	3	US-09-996-357-10
9	1225	97.2	232	3	US-09-389-782-1
10	1225	97.2	232	4	US-10-617-639-7
11	1225	97.2	232	4	US-10-761-593A-26
12	1225	97.2	232	5	US-10-831-622-97
13	1225	97.2	232	5	US-10-800-497-26
14	1225	97.2	232	5	US-10-800-449-26
15	1225	97.2	232	5	US-10-964-215-97
16	1225	97.2	232	6	US-11-016-518A-26
17	1225	97.2	232	6	US-11-017-185-26
18	1225	97.2	234	5	US-10-627-556-684
19	1225	97.2	235	4	US-10-207-655-208
20	1225	97.2	235	5	US-10-627-556-2
21	1225	97.2	235	5	US-10-734-661A-6
22	1225	97.2	247	3	US-09-996-357-13
23	1225	97.2	251	4	US-10-008-063-18
24	1225	97.2	251	4	US-10-152-363A-6
25	1225	97.2	267	3	US-09-996-357-12
26	1225	97.2	269	5	US-10-609-783B-50
27	1225	97.2	285	6	US-11-018-102-11

28	1225	97.2	288	3	US-09-822-851B-14	Sequence 14, Appl
29	1225	97.2	288	4	US-10-119-637A-14	Sequence 14, Appl
30	1225	97.2	288	6	US-11-018-102-1	Sequence 1, Appl
31	1225	97.2	288	6	US-11-129-083-14	Sequence 14, Appl
32	1225	97.2	288	6	US-11-128-495-14	Sequence 14, Appl
33	1225	97.2	288	6	US-11-128-496-14	Sequence 14, Appl
34	1225	97.2	288	6	US-11-129-080-14	Sequence 14, Appl
35	1225	97.2	288	6	US-11-128-709-14	Sequence 14, Appl
36	1225	97.2	329	4	US-10-370-749-48	Sequence 48, Appl
37	1225	97.2	329	5	US-10-798-380-37	Sequence 37, Appl
38	1225	97.2	330	3	US-09-995-898A-15	Sequence 15, Appl
39	1225	97.2	330	3	US-09-892-549-38	Sequence 38, Appl
40	1225	97.2	330	4	US-10-047-542-20	Sequence 20, Appl
41	1225	97.2	330	4	US-10-269-805-68	Sequence 68, Appl
42	1225	97.2	330	4	US-10-310-719-8	Sequence 8, Appl
43	1225	97.2	330	4	US-10-112-582-1	Sequence 1, Appl
44	1225	97.2	330	4	US-10-320-231A-81	Sequence 81, Appl
45	1225	97.2	330	4	US-10-383-902A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-847-208-3
; Sequence 3, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-3

Query Match	100.0%;	Score 1260;	DB 3;	Length 232;
Best Local Similarity	100.0%;	Pred. No. 1.1e-92;	Mismatches 0;	Indels 0; Gaps 0;
Matches	232;	Conservative	0;	
Qy	1	EPKSCDKHTCCPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	
Db	1	EPKSCDKHTCCPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	
Qy	61	NWYDGVGVHNVKTPREEQNSTYRVSVLTVLHQNMMNGKEYCKYKSNKALPAPIET	120	
Db	61	NWYDGVGVHNVKTPREEQNSTYRVSVLTVLHQNMMNGKEYCKYKSNKALPAPIET	120	
Qy	121	ISKAKVQPREQVYTLTPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180	
Db	121	ISKAKVQPREQVYTLTPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180	
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSPGK	232	
Db	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSPGK	232	

RESULT 2
US-10-000-439-3
; Sequence 3, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

Db	279	PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK	330
RESULT 4			
US-10-000-439-2			
; Sequence 2, Application US/10000439			
; Publication No. US20030064063A1			
; GENERAL INFORMATION:			
; APPLICANT: Saxon, Andrew			
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR			
; FILE REFERENCE: UC067.004A			
; CURRENT APPLICATION NUMBER: US/10/000,439			
; PRIOR FILING DATE: 2001-10-24			
; PRIOR APPLICATION NUMBER: US 09/847,208			
; PRIOR FILING DATE: 2001-05-01			
; NUMBER OF SEQ ID NOS: 13			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 2			
; LENGTH: 330			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-000-439-2			
Query Match 100.0%; Score 1260; DB 4; Length 330;			
Best Local Similarity 100.0%; Pred. No. 1.7e-92;			
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Db	99	EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	158
QY	61	NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIETK	120
Db	159	NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIETK	218
QY	121	ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTP	180
Db	219	ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTP	278
QY	181	PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK	232
Db	279	PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK	330
RESULT 5			
US-09-847-208-7			
; Sequence 7, Application US/09847208			
; Publication No. US20030082190A1			
; GENERAL INFORMATION:			
; APPLICANT: Saxon, Andrew			
; APPLICANT: Zhang, Ke			
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF			
; FILE REFERENCE: UC67.002A			
; CURRENT APPLICATION NUMBER: US/09/847,208			
; CURRENT FILING DATE: 2001-05-01			
; NUMBER OF SEQ ID NOS: 177			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 7			
; LENGTH: 569			
; TYPE: PRT			
; ORGANISM: Unknown			
; FEATURE:			
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4			
; OTHER INFORMATION: (Ige)			
US-09-847-208-7			
Query Match 100.0%; Score 1260; DB 3; Length 569;			
Best Local Similarity 100.0%; Pred. No. 3.2e-92;			
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 6

US-10-000-439-7
; Sequence 7, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3
; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (Ige) sequence
US-10-000-439-7

Query Match 100.0%; Score 1260; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 7

US-10-966-673-29
; Sequence 29, Application US/10966673
; Publication No. US20050226864A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R
; APPLICANT: Teurushita, Naoya
; TITLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
; FILE REFERENCE: 05882.0039.NPUS07
; CURRENT APPLICATION NUMBER: US/10/966,673

; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/562,627
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US 60/511,687
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 330
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-966-673-29

Query Match 97.5%; Score 1228; DB 5; Length 330;
Best Local Similarity 97.4%; Pred. No. 6.1e-90;
Matches 226; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 219 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 8

US-09-996-357-10
; Sequence 10, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Geffer, Malcolm L
; APPLICANT: Isreal, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; TREATING AN AMYLOIDOGENIC DISEASE
; FILE REFERENCE: PPT-105
; CURRENT APPLICATION NUMBER: US/09/996,357
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-357-10

Query Match 97.2%; Score 1225; DB 3; Length 232;
Best Local Similarity 97.0%; Pred. No. 7.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTPREEQNSTYRVSIVLTQLHQNMMNGKEYCKVSNKALPAPIEKT 120

121	QY	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180
121	Db	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180
181	QY	PVLDSVGSFPLYSKLTVDKSRWQOQNVPFCSCVMHEALHNYQQRSLSLSPGK	232
181	Db	PVLDSVGSFPLYSKLTVDKSRWQOQNVPFCSCVMHEALHNYQQRSLSLSPGK	232

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RESULT 9
US-09-389-782-1
; Sequence 1, Application US/09389782
; Publication No. US20030144187A1
; GENERAL INFORMATION:
; APPLICANT: Wooden, Scott K.
; APPLICANT: Mann, Michael B.
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods
; FILE REFERENCE: A-604
; CURRENT APPLICATION NUMBER: US/09/389,782
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human
US-09-389-782-1

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Query Match	97.2%	Score 1225;	DB 3;	Length 232;
Best Local Similarity	97.0%;	Pred. No. 7.1e-90;		
Matches 225; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	EPKSCDKTHTCCPCAPPELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	
Db	1	EPKSCDKTHTCCPCAPPELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	
Qy	61	NWYVDGVEVHNKTKPRREQNSTRYVVSIVLTVLHQNMNGKEYCKCKVSNKALPAPIEKT	120	
Db	61	NWYVDGVEVHNNAKTPREEQNSTRYVVSIVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT	120	
Qy	121	ISKAKVQPREPQVVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180	
Db	121	ISKAKGQPREPQVVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180	
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNFVSCSWMEAHLNHHYQQRSLSLSPGK	232	
Db	181	PVLDSGDSFFLYSKLTVDKSRWQQGNFVSCSWMEAHLNHHYQKRSLSLSPGK	232	

RESULT 10
 US-10-617-619-7
 ; Sequence 7, Application US/10617619
 ; Publication No. US20040110929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bjorn, Soren E
 ; APPLICANT: Nicolaisen, Else M
 ; APPLICANT: Jorgensen, Anker S
 ; TITLE OF INVENTION: Tf Binding Compound
 ; FILE REFERENCE: 6455.200-US
 ; CURRENT APPLICATION NUMBER: US/10/617,619
 ; CURRENT FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
 ; PRIOR FILING DATE: 2002-07-12
 ; PRIOR APPLICATION NUMBER: US 60/404,568
 ; PRIOR FILING DATE: 2002-08-19
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 7
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Human

US-10-617-619-7

	Query Match	97.23;	Score 1225;	DB 4;	Length 232;
	Best Local Similarity	97.08;	Pred. No. 7.1e-90;		
	Matches 225;	Conservative	3;	Mismatches 4;	Indels 0;
					Gaps 0;
Qy	1	EPKSCDXTHTCCPPCAPPELLGGPSVFLFPKPKD	TLMISRTPEVTCVVVDVSHEDPEVKF	60	
Db	1	EPKSCDXTHTCCPPCAPPELLGGPSVFLFPKPKD	TLMISRTPEVTCVVVDVSHEDPEVKF	60	
Qy	61	NWYVDGVEVHNKTKPRREQYNSTRYVSVLTVLHQ	NMNGKEYCKCKVSNKALPAPIEKT	120	
Db	61	NWYVDGVEVHNKTKPRREQYNSTRYVSVLTVLHQ	NMNGKEYCKCKVSNKALPAPIEKT	120	
Qy	121	ISKAQVOPREPQVYVTLPPSRDELTKNQVSLTCL	VKGFPSPDIAVEWESNGQPPENNYKTP	180	
Db	121	ISKAQVOPREPQVYVTLPPSRDELTKNQVSLTCL	VKGFPSPDIAVEWESNGQPPENNYKTP	180	
Qy	181	PVLDSVGSFFLYSKLTVDKRWQCGNVFSCSVM	HEALHNHYQOQSLSLSPGK	232	
Db	181	PVLDSVGSFFLYSKLTVDKRWQCGNVFSCSVM	HEALHNHYQOQSLSLSPGK	232	

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RESULT 11
US-10-761-593A-26
; Sequence 26, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-761-593A-26

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	Query Match	97.2%;	Score 1225;	DB 4;	Length 232;
	Best Local Similarity	97.0%;	Prod. No. 7.1e-90;		
	Matches 225;	Conservative	3;	Mismatches 4;	Indels 0; Gaps 0
Qy	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
Db	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
Qy	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNCKEYKCKVSNKALPAPIEKT	120		
Db	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT	120		
Qy	121	ISKAKGVPREPVQVTLTPSRDELTKNQVSLTCLVKGFYPSDIAVWESWNGQPPENNYKTP	180		
Db	121	ISKAKGVPREPVQVTLTPSRDELTKNQVSLTCLVKGFYPSDIAVWESWNGQPPENNYKTP	180		
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	232		
Db	181	PVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	232		

RESULT 12
US-10-831-622-97
; Sequence 97, Application US/10831622
; Publication No. US20040248257A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan

APPLICANT: Wilkinson, Beverley
; TITLE OF INVENTION: SEQUENCE COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: TSRI 810.1
; CURRENT APPLICATION NUMBER: US/10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-622-97

Query Match 97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

RESULT 13
US-10-800-497-26
; Sequence 26, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; TITLE OF INVENTION: stimulating factor with
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-10-800-497-26

Query Match 97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
RESULT 14
US-10-800-449-26
; Sequence 26, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-10-800-449-26

Query Match 97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

RESULT 15
US-10-964-215-97
; Sequence 97, Application US/10964215
; Publication No. US20050152893A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
; TITLE OF INVENTION: OF TRANSPLANT REJECTION
; FILE REFERENCE: TSRI 810.2
; CURRENT APPLICATION NUMBER: US/10/964,215
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-964-215-97

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Query Match      97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7.le-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPAPAPGLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPAPAPGLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQNMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQDNLNGKEYCKVSNKALPAPIEKT 120

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180

Qy 181 PVLDSVGSFELYSKLITVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 181 PVLDSGDSFELYSKLITVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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Search completed: November 30, 2005, 01:16:48
Job time : 98.087 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 01:10:40 ; Search time 4.62319 Seconds
(without alignments)
152.100 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCCPAPPELL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11 NEW PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	330	7 US-11-022-289-11	Sequence 11, Appl
2	1225	97.2	444	7 US-11-172-320-6	Sequence 6, Appl
3	1225	97.2	452	7 US-11-016-503-6	Sequence 6, Appl
4	1225	97.2	459	1 US-10-949-720-390	Sequence 390, App
5	1225	97.2	462	7 US-11-016-503-8	Sequence 8, Appl
6	1225	97.2	551	7 US-11-022-289-7	Sequence 7, Appl
7	1225	97.2	551	7 US-11-022-289-8	Sequence 8, Appl
8	1225	97.2	557	7 US-11-016-503-4	Sequence 4, Appl
9	1225	97.2	557	7 US-11-022-289-4	Sequence 4, Appl
10	1225	97.2	557	7 US-11-022-289-5	Sequence 5, Appl
11	1225	97.2	557	7 US-11-022-289-6	Sequence 6, Appl
12	1225	97.2	567	7 US-11-016-503-2	Sequence 2, Appl
13	1225	97.2	567	7 US-11-016-503-10	Sequence 10, Appl
14	1225	97.2	771	1 US-10-949-720-389	Sequence 389, App
15	1220	96.8	489	1 US-10-835-475-11	Sequence 11, Appl
16	1220	96.8	514	1 US-10-835-475-2	Sequence 2, Appl
17	1219	96.7	330	7 US-11-022-289-1	Sequence 1, Appl
18	1219	96.7	548	7 US-11-022-289-3	Sequence 3, Appl
19	1219	96.7	557	7 US-11-022-289-2	Sequence 2, Appl
20	1219	96.7	564	7 US-11-022-289-10	Sequence 10, Appl
21	1219	96.7	579	7 US-11-174-186-41	Sequence 41, Appl
22	1198	95.1	531	7 US-11-008-727-18	Sequence 18, Appl
23	1195	94.8	455	7 US-11-016-503-14	Sequence 14, Appl
24	1195	94.8	458	7 US-11-016-503-12	Sequence 12, Appl
25	1195	94.8	458	7 US-11-016-503-16	Sequence 16, Appl

26	1189	94.4	227	7 US-11-008-727-14	Sequence 14, Appl
27	1176	93.3	430	7 US-11-016-503-17	Sequence 17, Appl
28	1107	87.9	326	7 US-11-144-248-28	Sequence 28, Appl
29	1107	87.9	470	7 US-11-144-248-45	Sequence 45, Appl
30	1107	87.9	470	7 US-11-144-248-46	Sequence 46, Appl
31	1107	87.9	470	7 US-11-144-248-49	Sequence 49, Appl
32	1107	87.9	473	7 US-11-144-248-50	Sequence 50, Appl
33	1104	87.6	450	7 US-11-025-712-12	Sequence 12, Appl
34	776	61.6	236	7 US-11-008-727-4	Sequence 4, Appl
35	776	61.6	470	7 US-11-008-727-20	Sequence 20, Appl
36	776	61.6	476	7 US-11-008-727-22	Sequence 22, Appl
37	776	61.6	509	7 US-11-008-727-16	Sequence 16, Appl
38	371.5	29.5	312	1 US-10-723-207-2	Sequence 2, Appl
39	333	26.4	325	1 US-10-723-207-1	Sequence 1, Appl
40	332.5	26.4	313	1 US-10-723-207-3	Sequence 3, Appl
41	330.5	26.2	313	1 US-10-723-207-4	Sequence 4, Appl
42	251	19.9	353	7 US-11-022-289-9	Sequence 9, Appl
43	241.5	19.2	236	7 US-11-022-289-12	Sequence 12, Appl
44	155	12.3	105	7 US-11-025-712-6	Sequence 6, Appl
45	151	12.0	230	1 US-10-894-730-371	Sequence 371, App

ALIGNMENTS

RESULT 1

US-11-022-289-11
; Sequence 11, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-289-11

Query Match 97.2%; Score 1225; DB 7; Length 330;

Best Local Similarity 97.0%; Pred. No. 1e-98;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	1	EPKSCDKTHTCCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
DB	99	EPKSCDKTHTCCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKF	158
QY	61	NWYDGVGEVHNKTPREEQYNSTYRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKT	120
DB	159	NWYDGVGEVHNKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKT	218
QY	121	ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP	180
DB	219	ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP	278
QY	181	PVLDSGSGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK	232
DB	279	PVLDSGSGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK	330

RESULT 2

US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke

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; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-132-320-6

Query Match          97.2%; Score 1225; DB 7; Length 444;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 213 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 272

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 120
Db 273 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 332

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 333 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 392

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 232
Db 393 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 444

RESULT 3
US-11-016-503-6
; Sequence 6, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-6

Query Match          97.2%; Score 1225; DB 7; Length 452;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 228 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 287

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 120
Db 288 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 347

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 407

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 232
Db 408 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 459

RESULT 5
US-11-016-503-8
; Sequence 8, Application US/11016503
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Qy 1 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 221 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 280

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 120
Db 281 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 340

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 341 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 400

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 232
Db 401 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 452

RESULT 4
US-10-949-720-390
; Sequence 390, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Kraasoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC-FC protein
US-10-949-720-390

Query Match          97.2%; Score 1225; DB 1; Length 459;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 228 EPKSCDKTHTCCPPCAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 287

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 120
Db 288 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 347

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 407

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 232
Db 408 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 459

RESULT 5
US-11-016-503-8
; Sequence 8, Application US/11016503
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Publication No. US20050245447A1
GENERAL INFORMATION:
APPLICANT: Nicholas J. Papadopoulos et al.
TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
CURRENT APPLICATION NUMBER: US/11/016,503
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/009,852
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/138,133
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
US-11-016-503-8

Query Match          97.2%; Score 1225; DB 7; Length 462;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 231 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 290
QY 61 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 291 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 350
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 351 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 410
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNNHYTQKLSLSLSPGK 232
DB 411 PVLDSGSGFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNNHYTQKLSLSLSPGK 462

RESULT 6
US-11-022-289-7
Sequence 7, Application US/11022289
Publication No. US20050249723A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 551
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
US-11-022-289-7

Query Match          97.2%; Score 1225; DB 7; Length 551;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 159 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNNHYTQKLSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNNHYTQKLSLSLSPGK 330

RESULT 7
US-11-022-289-8
Sequence 8, Application US/11022289
Publication No. US20050249723A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8
LENGTH: 551
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
US-11-022-289-8

Query Match          97.2%; Score 1225; DB 7; Length 551;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 159 NWYDGVGVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNNHYTQKLSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNNHYTQKLSLSLSPGK 330

RESULT 8
US-11-016-503-4
Sequence 4, Application US/11016503
Publication No. US20050245447A1
GENERAL INFORMATION:
APPLICANT: Nicholas J. Papadopoulos et al.
TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
CURRENT APPLICATION NUMBER: US/11/016,503
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/009,852
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2000-05-23
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QY 61 NWYDGVVHNVKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 159 NWYDGVVHNAKTTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 330

RESULT 12
US-11-016-503-2
; Sequence 2, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-2

Query Match 97.2%; Score 1225; DB 7; Length 567;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHTCCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 336 EPKSCDKHTHTCCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 395
QY 61 NWYDGVVHNVKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 396 NWYDGVVHNAKTTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 455
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 456 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 515
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 516 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 567

RESULT 13
US-11-016-503-10
; Sequence 10, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-10

Query Match 97.2%; Score 1225; DB 7; Length 567;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHTCCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 336 EPKSCDKHTHTCCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 395
QY 61 NWYDGVVHNVKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 396 NWYDGVVHNAKTTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 455
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 456 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 515
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 516 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 567

RESULT 14
US-10-949-720-389
; Sequence 389, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Kraenoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B4ECV3-FC protein
US-10-949-720-389

Query Match 97.2%; Score 1225; DB 1; Length 771;
Best Local Similarity 97.0%; Pred. No. 2.8e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKHTHTCCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 540 EPKSCDKHTHTCCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 599

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:34:13 ; Search time 152.464 Seconds
(without alignment)
922.194 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPPTVKILQSSCDGGGHP.....HEAASPQTQVORAVSNVPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a
-score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707	100.0	320	AAO19667	Aao19667 Human Ige
2	1707	100.0	323	AAU80286	Aau80286 Human Ige
3	1707	100.0	323	AAU80285	Aau80285 Human Ige
4	1707	100.0	323	AAU80284	Aau80284 Human Ige
5	1707	100.0	324	AAR83559	Aar83559 Fc(epsilo
6	1707	100.0	325	AAR75225	Aar75225 Human Ige
7	1707	100.0	325	AAR77241	Aar77241 Human Ige
8	1707	100.0	327	ADY21849	Ady21849 Human Ige
9	1707	100.0	331	AAE03642	Aae03642 Human Ige
10	1707	100.0	331	ADD25768	Add25768 Binding d
11	1707	100.0	331	ADY21799	Ady21799 Human Ige
12	1707	100.0	331	ADY21722	Ady21722 Human Ige
13	1707	100.0	367	AAEP80291	Aape80291 Interleuk
14	1707	100.0	427	AAO19666	Aao19666 Human Ige
15	1707	100.0	428	AAAM47863	Aam47863 Human Ig-
16	1707	100.0	428	AAU80283	Aau80283 Human Ige
17	1707	100.0	428	AAAM50940	Aam50940 Human Ige
18	1707	100.0	428	AAE35113	Aae35113 Human imm
19	1707	100.0	428	ADD48440	Add48440 Human pro
20	1707	100.0	428	ADY97382	Ady97382 Human Ige
21	1707	100.0	569	AAO19668	Aao19668 GE2 fusio
22	1707	100.0	574	ABG94250	Abg94250 Human Ige
23	1707	100.0	574	ABG80562	Abg80562 Human Ige
24	1707	100.0	574	ABP96592	Abp96592 Human Ige

25	1707	100.0	574	7	ADE97368	Ade97368 Human imm
26	1707	100.0	586	9	ADY22009	Ady22009 Antibody
27	1707	100.0	592	7	ADD25773	Add25773 Binding d
28	1707	100.0	592	9	ADY21754	Ady21754 Antibody
29	1707	100.0	593	9	ADY21873	Ady21873 Antibody
30	1707	100.0	635	9	ADY21801	Ady21801 Antibody
31	1707	100.0	648	9	ADY21805	Ady21805 Antibody
32	1707	100.0	648	9	ADY21809	Ady21809 Antibody
33	1701	99.6	325	3	AAV79994	Aav79994 Human imm
34	1696	99.4	336	5	AAU80288	Aau80288 Human Ige
35	1696	99.4	441	5	AAU80287	Aau80287 Human Ige
36	1695.5	99.3	497	9	ADW24784	Adw24784 Human var
37	1695.5	99.3	497	9	ADW24742	Adw24742 Human var
38	1695.5	99.3	497	9	ADZ08809	Adz08809 Mammalian
39	1695.5	99.3	497	9	ADZ08940	Adz08940 Mammalian
40	1695.5	99.3	497	9	ADZ44466	Adz44466 Human imm
41	1695.5	99.3	497	9	AEA16541	Aea16541 Human MCP
42	1695.5	99.3	497	9	ABE72776	AbE72776 Anti-Ltal
43	1693	99.2	493	1	AAAP40065	Aap40065 Sequence
44	1685	98.7	325	2	AAR83582	Aar83582 CH2 to CH
45	1677	98.2	315	2	AAR85582	Aar85582 Fc(epsilo

ALIGNMENTS

RESULT 1

AAO19667

ID AAO19667 standard; protein; 320 AA.

XX

XX AAO19667;

XX

XX 28-MAR-2003 (first entry)

XX

XX Human Ige heavy chain constant region CH2-CH3-CH4 portion.

XX

XX Human; Ige; immunoglobulin E; immunotherapy; immune disease;

XX Fcepsilon receptor; autoimmune disease; constant region; heavy chain;

XX antiasthmatic; antiallergic; antiinflammatory; dermatological;

XX antiarthritic; antirheumatic; antidiabetic; neuroprotective;

XX CH2-CH3-CH4 region.

XX Homo sapiens.

XX

XX WO200288317-A2.

XX

XX 07-NOV-2002.

XX

XX 01-MAY-2002; 2002WO-US013527.

XX

XX 01-MAY-2001; 2001US-00847208.

XX 24-OCT-2001; 2001US-00000439.

XX (REGC) UNIV CALIFORNIA.

XX Saxon A, Zhang K, Zhu D;

XX WPI; 2003-103456/09.

XX

XX New fusion molecules comprising polypeptide sequences that bind to IgG
inhibitory receptor and native IGE receptor, useful for treating IGE-
mediated hypersensitivity reactions, e.g. asthma or allergies, or
autoimmune diseases.

XX

XX Claim 21; Fig 6; 116pp; English.

XX

XX The present invention relates to a fusion molecule comprising a first
polypeptide sequence capable of specific binding to a native IGE
inhibitory receptor consisting of an immune receptor tyrosine-based
inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
functionally connected to a second polypeptide sequence capable of
specific binding directly or indirectly to a native IGE receptor
(FcepsilonR). Also provided are nucleotide sequences encoding such a

CC fusion protein. The fusion molecules and compositions are useful for
CC treating an Ige-mediated biological response, preferably an Ige-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human Ige
CC heavy chain constant region CH2-CH3-CH4 portion
XX
SQ Sequence 320 AA;

Query Match 100.0%; Score 1707; DB 6; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.1e-129; Mismatches 0; Gaps 0;
Matches 320; Conservative 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
Db 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60

QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120

QY 121 LFRKSPITITCLVVDLAPSGTGNLTWSRSGKPNVHSTRKEKQKNGTLTVTSTLPVGT 180
Db 121 LFRKSPITITCLVVDLAPSGTGNLTWSRSGKPNVHSTRKEKQKNGTLTVTSTLPVGT 180

QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240

QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEFICRAV 300
Db 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEFICRAV 300

QY 301 HEAASPSQTVQRAVSNPGK 320
Db 301 HEAASPSQTVQRAVSNPGK 320

RESULT 2
AAU80286
ID AAU80286 standard; protein; 323 AA.
XX
AC AAU80286;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human Ige C2-C3-C4 domains for E.Coli expression.
XX
KW Ige; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; Ige;
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KW heavy chain C domain.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200220038-A2.
XX
PD 14-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-DK000579.
XX
PR 06-SEP-2000; 2000DK-00001326.
PR 15-SEP-2000; 2000US-0232831P.
XX
PA (PHAR-) PHARMEXA AS.
XX
PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;
XX
XX WPI; 2002-383033/41.
DR

DR N-PSDB; ABK511134.
XX
XX Inducing immune response against autologous immunoglobulin E in an
PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
PT epitope an/or B-cell epitope derived from the immunoglobulin.
XX
PS Disclosure; Page 112-113; 151pp; English.
XX
XX This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (Ige) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes of
CC the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response against
CC autologous Ige in an animal, which is useful for downregulating
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC asthma and atopic dermatitis. The present sequence represents the human
CC Ige heavy chain C2-C3-C4 domains optimised for expression in an E. Coli
CC system, this sequence was used to create the epitopes of the invention
XX
SQ Sequence 323 AA;

Query Match 100.0%; Score 1707; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 4.2e-129; Mismatches 0; Gaps 0;
Matches 320; Conservative 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60
Db 4 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 63

QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db 64 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 123

QY 121 LFRKSPITITCLVVDLAPSGTGNLTWSRSGKPNVHSTRKEKQKNGTLTVTSTLPVGT 180
Db 124 LFRKSPITITCLVVDLAPSGTGNLTWSRSGKPNVHSTRKEKQKNGTLTVTSTLPVGT 183

QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 184 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243

QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEFICRAV 300
Db 244 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEFICRAV 303

QY 301 HEAASPSQTVQRAVSNPGK 320
Db 304 HEAASPSQTVQRAVSNPGK 323

RESULT 3
AAU80285
ID AAU80285 standard; protein; 323 AA.
XX
AC AAU80285;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human Ige C2-C3-C4 domains for mammalian expression.
XX
KW Ige; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; Ige;
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KW heavy chain C domain.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200220038-A2.
DR

XX 14-MAR-2002.
PD
XX
XX 06-SEP-2001; 2001WO-DK000579.
PF
XX
XX 06-SEP-2000; 2000DK-00001326.
PR
XX
XX 15-SEP-2000; 2000US-0232831P.
PR
XX
XX (PHAR-) PHARMEXA AS.
PA
XX
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;
PI
XX
XX WPI; 2002-383033/41.
DR
XX
XX N-PSDB; ABK51133.
DR
XX
XX Inducing immune response against autologous immunoglobulin E in an
PT
XX animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
PT
XX epitope an/or B-cell epitope derived from the immunoglobulin.
PT
XX
XX Disclosure; Page 108-110; 151pp; English.
PS
XX
XX This invention relates to a novel method for inducing an immune response
CC
XX against autologous immunoglobulin E (IgE) in an animal. The method
CC
XX comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC
XX (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
CC
XX epitope (TH epitope) which is foreign to the animal, by antigen
CC
XX presenting cells (APCs) of the animal's immune system. The epitopes of
CC
XX the invention may be used as a vaccine against allergic diseases. The
CC
XX method of the invention is useful for inducing an immune response against
CC
XX autologous IgE in an animal, which is useful for downregulating
CC
XX autologous IgE in the animal. This method is useful in the prevention and
CC
XX treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC
XX asthma and atopic dermatitis. The present sequence represents the human
CC
XX IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian
CC
XX system, this sequence was used to create the epitopes of the invention
XX
XX Sequence 323 AA;
SQ

Query Match 100.0%; Score 1707; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 4.2e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGTTINITWLEDQGVMDVLDLSTASTQOE 60
Db 4 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGTTINITWLEDQGVMDVLDLSTASTQOE 63

Qy 61 GELASTQSELTLSQKHLSDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 120
Db 64 GELASTQSELTLSQKHLSDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSFD 123

Qy 121 LFIRKSPITICLVVDLAPSKGTVNLTWGRASGKPVNHSRKEKQNGTLTWTSTLPVGT 180
Db 124 LFIRKSPITICLVVDLAPSKGTVNLTWGRASGKPVNHSRKEKQNGTLTWTSTLPVGT 183

Qy 181 RDWIEGETYQCHVTPLPLALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 184 RDWIEGETYQCHVTPLPLALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTLACLIQ 243

Qy 241 NFMPEDISVQHLNHEVQLPDARHSTTPQPKTKGSGFFVFSRLVTRAEWEQKDEFICRAV 300
Db 244 NFMPEDISVQHLNHEVQLPDARHSTTPQPKTKGSGFFVFSRLVTRAEWEQKDEFICRAV 303

Qy 301 HEAASPSQTVQRAVSNPKG 320
Db 304 HEAASPSQTVQRAVSNPKG 323

RESULT 4
AAU80284
ID AAU80284 standard; protein; 323 AA.
XX
AC AAU80284;
XX

DT 30-JUL-2002 (first entry)
XX Human IgE heavy chain C2-C3-C4 domains.
DE
XX
XX IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KW heavy chain C domain.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 8..103
FT /note= "IGE heavy chain C2 domain"
FT Region 100..114
FT /note= "Epitope including C2C3 linker"
FT Region 104..111
FT /note= "Linker between domains C2 and C3"
FT Domain 112..211
FT /label= IGE heavy chain C3 domain
FT Region 139..145
FT /note= "Epitope in BC loop"
FT Region 167..175
FT /note= "Epitope in DE loop"
FT Domain 196..206
FT /note= "Epitope in FG loop"
FT Region 210..218
FT /note= "Epitope including C3C4 linker"
FT Region 212..215
FT /note= "Linker between domains C3 and C4"
FT Domain 216..317
FT /note= "IGE heavy chain C4 domain"
XX WO200220038-A2.
XX 14-MAR-2002.
XX 06-SEP-2001; 2001WO-DK000579.
XX 06-SEP-2000; 2000DK-00001326.
PR 15-SEP-2000; 2000US-0232831P.
XX (PHAR-) PHARMEXA AS.
PA Klysner S, Von Hoegen P, Voldborg B, Gautam A;
PI WPI; 2002-383033/41.
XX Inducing immune response against autologous immunoglobulin E in an
DR animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
PT epitope an/or B-cell epitope derived from the immunoglobulin.
PT
XX Disclosure; Page 105-106; 151pp; English.
PS
XX This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (IgE) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes of
CC the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response against
CC autologous IgE in an animal, which is useful for downregulating
CC autologous IgE in the animal. This method is useful in the prevention and
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC asthma and atopic dermatitis. The present sequence represents the human
CC IgE heavy chain C2-C3-C4 domains used to create the epitopes of the
CC invention
XX
XX Sequence 323 AA;
SQ

Query Match 100.0%; Score 1707; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 4.2e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

FT /label= Aen394
FN /note= "glycosylation site"
XX
XX WO9514779-A1.
XX
XX 01-JUN-1995.
XX
XX 22-NOV-1994; 94WO-GB002561.
XX
XX 22-NOV-1993; 93GB-00024013.
XX
XX (THRE-) 3I RES EXPL LTD.
XX (CLLT ) CELLTech THERAPEUTICS LTD.
XX
XX Gould HJ, Young RJ, Sutton BJ, Owens RJ;
XX
XX WPI; 1995-206936/27.
XX N-PSDB; AAQ87474.
XX
XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc - useful
XX to study and treat allergy.
XX
XX Disclosure; Page 6; 55pp; English.
XX
XX The sequence represents a mutant sequence of a human IgE-Fc chain (amino
XX acids 224-547) which is of sufficient length to bind Fc-epsilon RI and/or
XX Fc-epsilon FII IgE receptor sites on human cells. The protein is useful
XX in the study and treatment of allergy. (Updated on 25-MAR-2003 to correct
XX PN field.)
XX
XX Sequence 325 AA;
XX
XX Query Match 100.0%; Score 1707; DB 2; Length 325;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-129;
XX Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVDLSTASTTQE 60
XX DB 6 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVDLSTASTTQE 65
XX
XX QY 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRPSFD 120
XX DB 66 GELASTQSELTLSQKHWSLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRPSFD 125
XX
XX QY 121 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGPNVHSTRKEEKQKNGTLTSTLPVGT 180
XX DB 126 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGPNVHSTRKEEKQKNGTLTSTLPVGT 185
XX
XX QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
XX DB 186 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245
XX
XX QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 300
XX DB 246 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 305
XX
XX QY 301 HEAASPSQTVQRAVSNPGK 320
XX DB 306 HEAASPSQTVQRAVSNPGK 325
XX
XX RESULT 7
XX ID AAR77241 standard; protein; 325 AA.
XX AC AAR77241;
XX XX
XX XX 25-MAR-2003 (revised)
XX DT 10-NOV-1995 (first entry)
XX XX
XX DE Human IgE Fc chain (amino acids 224-547) wild-type sequence.
XX XX
XX KW IgE Fc fragment; antiallergic.

```

```

XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 149 /label= Aen371
XX FT /note= "glycosylation site"
XX
XX Misc-difference 172 /label= Aen394
XX FT /note= "glycosylation site"
XX
XX WO9514779-A1.
XX
XX 01-JUN-1995.
XX
XX 22-NOV-1994; 94WO-GB002561.
XX
XX 22-NOV-1993; 93GB-00024013.
XX
XX (THRE-) 3I RES EXPL LTD.
XX (CLLT ) CELLTech THERAPEUTICS LTD.
XX
XX Gould HJ, Young RJ, Sutton BJ, Owens RJ;
XX
XX WPI; 1995-206936/27.
XX N-PSDB; AAQ91170.
XX
XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc - useful
XX to study and treat allergy.
XX
XX Disclosure; Page 35-36; 55pp; English.
XX
XX The sequence represents the wild-type sequence of a human IgE-Fc chain
XX (amino acids 224-547) which is of sufficient length to bind Fc-epsilon RI
XX and/or Fc-epsilon FII IgE receptor sites on human cells. The sequence is
XX preferably mutated (see AAR75225) to represent a protein encoding a
XX protein where Cys225 is mutated, optionally together with Val224, Ser226
XX and Arg227. The protein is useful in the study and treatment of allergy.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 325 AA;
XX
XX Query Match 100.0%; Score 1707; DB 2; Length 325;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-129;
XX Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVDLSTASTTQE 60
XX DB 6 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVDLSTASTTQE 65
XX
XX QY 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRPSFD 120
XX DB 66 GELASTQSELTLSQKHWSLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRPSFD 125
XX
XX QY 121 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGPNVHSTRKEEKQKNGTLTSTLPVGT 180
XX DB 126 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGPNVHSTRKEEKQKNGTLTSTLPVGT 185
XX
XX QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
XX DB 186 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245
XX
XX QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 300
XX DB 246 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 305
XX
XX QY 301 HEAASPSQTVQRAVSNPGK 320
XX DB 306 HEAASPSQTVQRAVSNPGK 325
XX
XX RESULT 8
XX ADY21849

```

ADY21849 standard; protein; 327 AA.
ADY21849;
05-MAY-2005 (first entry)
Human IgE CH2-CH3-CH4 region.
Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;
antibody engineering; cancer; neoplasm; cytostatic; immune disorder;
graves disease; antithyroid; endocrine disease; hashimoto's disease;
immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;
inflammation; musculoskeletal disease; systemic lupus erythematosus;
inflammatory; musculoskeletal; dermatological disease;
metabolic disorder; sjogren's syndrome; ocular disease;
thrombocytopenic purpura; hemostatic; hematological disease;
multiple sclerosis; neuroprotective; neurological disease;
myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;
fungicide; viral infection; virucide; parasitic infection; antiparasitic;
fusion protein.
Homo sapiens.
WO2005017148-A1.
24-FEB-2005.
24-DEC-2003; 2003WO-US041600.
26-JUL-2003; 2003US-00627556.
(TRUB-) TRUBION PHARM INC.
Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
WPI; 2005-182370/19.
N-PSDB; ADY21848.
New non-naturally occurring single chain protein comprising polypeptides
with binding domain, connecting regions and N-terminally truncated
immunoglobulin, having immunological activity, useful for neutralizing
infectious agent.
Disclosure; Page 365; 590pp; English.
The invention relates to a non-naturally occurring single chain protein
comprising a first polypeptide having a binding domain polypeptide
capable of binding to a target molecule, the binding domain polypeptide
comprising a heavy chain variable region, which comprises an amino acid
substitution or deletion at one or more amino acid residues, a second
polypeptide comprising a connecting region attached to the first
polypeptide, and a third polypeptide comprising an N-terminally truncated
immunoglobulin heavy chain constant region polypeptide attached to the
second polypeptide, where the non-naturally occurring single-chain
protein is capable of an immunological activity. Also included are
reducing a target cell population in a subject (involving administering
to the subject a protein that is less than 150 kD, which involves
treating the target cell population with a first protein or peptide that
binds to cells within the target cell population, and treating the target
cell population with a second protein or peptide that capable of at least
one of binding an Fc receptor, inducing target cell apoptosis, or fix
complements, where the first protein or peptide molecule is directly
connected to the second protein or peptide molecule or, optionally, the
first protein or peptide molecule and the second protein or peptide
molecule are linked by a third protein or peptide molecule, and where the
protein molecule is not an antibody, a member of the TNF family or the
TNF receptor family, and is not conjugated with a bacterial toxin, a
cytotoxic drug, or a radioisotope), depleting cells in an animal
(involving administering a modified IGE protein into the blood stream of
an animal), a polynucleotide that encodes the polypeptide of the
invention, a cell containing the polynucleotide, a recombinant vector
capable of expressing the polypeptide, expressing the polypeptide, a
composition comprising the polypeptide) in combination with one or more

CC additional therapeutic compounds, displaying recombinant molecules (which
CC molecules include a native or engineered immunoglobulin heavy chain
CC variable region, the improvement comprising an immunoglobulin heavy chain
CC region that includes one or more mutation, substitution, alteration,
CC and/or deletion at one or more amino acid residue corresponding to
CC positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable
CC region) and a non-naturally occurring single chain antigen-binding
CC protein comprising protein having a mutation chosen from a list given in
CC the specification. The polypeptides of the invention comprise single
CC chain antibodies (scFv, with or without mutated residues) linked via an
CC immunoglobulin hinge region (wild-type or mutants where the cysteines are
CC changed to serines/prolines and denoted (SSS-P/H, (CSC-S)H etc) to an
CC immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which
CC may also have mutations in CH2 (e.g. F256N) or a truncated CH3 (e.g. F4
CC CH3, a 4 amino acid deletion). The polypeptide may be further linked to a
CC non-antibody protein such as the transmembrane and cytoplasmic tail
CC (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are
CC useful for neutralization of an infectious agent (where the infectious
CC agent is a bacterium, a virus, a parasite, or a fungus) and also for
CC treatment of cancer, immune disorders, Grave's disease, Hashimoto's
CC disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's
CC syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia
CC gravis. The present sequence is an antibody peptide or fragment (scFv,
CC hinge, CH region, VL or VH) used in a fusion protein of the invention.
XX
SQ Sequence 327 AA;
Query Match 100.0%; Score 1707; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.3e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60
DB 8 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 67
QY 61 GELASTQSELTLSQKHWSLDRTYTCQVYQGHFTFEDSTKCKADSNPRGVSAYLSRSPFD 120
DB 68 GELASTQSELTLSQKHWSLDRTYTCQVYQGHFTFEDSTKCKADSNPRGVSAYLSRSPFD 127
QY 121 LFIKSPITITCLVVDLAPSKGTVNLTWSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
DB 128 LFIKSPITITCLVVDLAPSKGTVNLTWSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 187
QY 181 RDWIEGETVQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
DB 188 RDWIEGETVQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300
DB 248 NFMPEDISVQWLHNEVQLPDARHSTTPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 307
QY 301 HEAASPSQTVQRAVSNPGK 320
DB 308 HEAASPSQTVQRAVSNPGK 327
RESULT 9
AAB03642
ID AAB03642 standard; protein; 331 AA.
AC AAB03642;
XX
XX 22-NOV-2000 (first entry)
XX Human IgE heavy chain constant regions 2, 3 and 4.
DE Human IgE heavy chain constant regions 2, 3 and 4.
XX Human; immunoglobulin E; IgE, vaccination; infection; allergy; asthma;
KW eczema; immunogenic peptide.
XX Homo sapiens.
XX WO200025722-A2.
PN
XX

PD 11-MAY-2000.
XX 21-OCT-1999; 99WO-SE001896.
XX 02-NOV-1998; 98US-0106652P.
PR 22-SEP-1999; 99US-00401636.
XX (RESI-) RESISTENTIA PHARM AB.
XX Hellman LT;
XX WPI; 2000-365342/31.
XX WPI; 2000-365342/31.
XX Immunogenic polypeptides useful for preventing the harmful effects of
PT immunoglobulin E in mammals.
XX Disclosure; Fig 1; 50pp; English.
XX The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2, 3 and 4 of the human IgE. It was used to
CC construct a number of immunogenic peptides which consisted of regions of
CC IgE from different mammals, which appear to cause a stronger polyclonal
CC anti-self IgE response than peptides consisting of the same regions from
CC one mammal. Immunogenic peptides, particularly those consisting of
CC different heavy chain constant regions, can be used for vaccination in
CC humans, against bacterial and viral infections and allergies, such as
CC asthma, fur, pollen and food allergies and eczema
XX
XX Sequence 331 AA;
Query Match 100.0%; Score 1707; DB 3; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.3e-129; Mismatches 0; Indels 0; Gaps 0;
Matches 320; Conservative 0;
QY 1 FTPTVKILQSCDCGGHFPPTIQLLCVSGYTPGTINITWLEDQVMDVDLSTASTTQEE 60
DB 12 FTPTVKILQSCDCGGHFPPTIQLLCVSGYTPGTINITWLEDQVMDVDLSTASTTQEE 71
QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRPSPPD 120
DB 72 GELASTQSELTLSQKHWSLDRYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRPSPPD 131
QY 121 LFIRKSPITCLVLDLAPSKGVNLTWRSRASKPNVHSTRKEEKQKNGTLTSTLPGVT 180
DB 132 LFIRKSPITCLVLDLAPSKGVNLTWRSRASKPNVHSTRKEEKQKNGTLTSTLPGVT 191
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPWPGRDKRTIACLIQ 240
DB 192 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPWPGRDKRTIACLIQ 251
QY 241 NFMPEDISVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWQKDEPICRAV 300
DB 252 NFMPEDISVQMLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWQKDEPICRAV 311
QY 301 HEAASPSQTVQRAVSNPK 320
DB 312 HEAASPSQTVQRAVSNPK 331
RESULT 10
ADD25768
ID ADD25768 standard; protein; 331 AA.
AC ADD25768;
XX
DT 15-JAN-2004 (first entry)
XX Binding domain-immunoglobulin fusion protein-associated protein #152.
DE Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX Unidentified.
XX US2003118592-A1.
XX 26-JUN-2003.
XX 25-JUL-2002; 2002US-00207655.
XX 17-JAN-2001; 2001US-0367358P.
XX 17-JAN-2002; 2002US-00053530.
XX 03-JUN-2002; 2002US-0385691P.
XX (GENE-) GENE-CRAFT INC.
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX WPI; 2003-801317/75.
XX New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX Disclosure; SEQ ID NO 329; 157pp; English.
XX The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising fixation. The
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX Sequence 331 AA;
Query Match 100.0%; Score 1707; DB 7; Length 331;
XX

Best Local Similarity 100.0%; Pred. No. 4.3e-129; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	FTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLBDGQVMDVLDLSTASTTQE 60
DB	8	FTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLBDGQVMDVLDLSTASTTQE 67
QY	61	GELASTQSELTLSQKHWSLDRITTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120
DB	68	GELASTQSELTLSQKHWSLDRITTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 127
QY	121	LFIRKSPPTITCLVLDLAPSKGTVNLWTSRASGKPVNHSRKEKQNGTLTVTSTLPVGT 180
DB	128	LFIRKSPPTITCLVLDLAPSKGTVNLWTSRASGKPVNHSRKEKQNGTLTVTSTLPVGT 187
QY	181	RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
DB	188	RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247
QY	241	NFMPEDISVQWLNEVQLDPARISTTOPRTKSGSGFFVFSRLVTRAWEQKDEFTICRAV 300
DB	248	NFMPEDISVQWLNEVQLDPARISTTOPRTKSGSGFFVFSRLVTRAWEQKDEFTICRAV 307
QY	301	HEAASPSQTVQRAVSNPGK 320
DB	308	HEAASPSQTVQRAVSNPGK 327
RESULT 11		
ADY21799		
ID	ADY21799	standard; protein; 331 AA.
XX	AC	ADY21799;
XX	DT	05-MAY-2005 (first entry)
XX	DE	Human IGE Fc (CH2-CH3-CH4) protein.
XX	KW	Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;
KW		antibody engineering; cancer; neoplasm; cytostatic; immune disorder;
KW		grave disease; antithyroid; endocrine disease; hashimoto's disease;
KW		immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;
KW		inflammation; musculoskeletal disease; systemic lupus erythematosus;
KW		antiinflammatory; dermatological; dermatological disease;
KW		metabolic disorder; Sjogren's syndrome; ocular disease;
KW		thrombocytopenic purpura; hemostatic; neurological disease;
KW		multiple sclerosis; neuroprotective; bacterial infection; fungal infection;
KW		myasthenia gravis; muscular-gen.; parasitic infection; antiparasitic;
KW		fusion protein.
XX	OS	Homo sapiens.
XX	XX	W02005017148-A1.
XX	PN	24-FEB-2005.
XX	PD	
XX	XX	24-DEC-2003; 2003WO-US041600.
XX	XX	26-JUL-2003; 2003US-00627556.
XX	PR	
XX	PA	(TRUB-) TRUBION PHARM INC.
XX	XX	Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX	PI	
XX	XX	WPI; 2005-182370/19.
XX	DR	N-PSDB; ADY21798.
XX	DR	
XX	XX	New non-naturally occurring single chain protein comprising polypeptides
PT		with binding domain, connecting regions and N-terminally truncated
PT		immunoglobulin, having immunological activity, useful for neutralizing
PT		infectious agent.

PS	Disclosure; Page 352; 590pp; English.	
XX		
CC	The invention relates to a non-naturally occurring single chain protein	
CC	(I) comprising a first polypeptide having a binding domain polypeptide	
CC	capable of binding to a target molecule, the binding domain polypeptide	
CC	comprising a heavy chain variable region, which comprises an amino acid	
CC	substitution or deletion at one or more amino acid residues, a second	
CC	polypeptide comprising a connecting region attached to the first	
CC	polypeptide, and a third polypeptide comprising an N-terminally truncated	
CC	immunoglobulin heavy chain constant region polypeptide attached to the	
CC	second polypeptide, where the non-naturally occurring single-chain	
CC	protein is capable of an immunological activity. Also included are	
CC	reducing a target cell population in a subject (involving administering	
CC	to the subject a protein that is less than 150 kD, which involves	
CC	treating the target cell population with a first protein or peptide that	
CC	binds to cells within the target cell population, and treating the target	
CC	cell population with a second protein or peptide that capable of at least	
CC	one of binding an Fc receptor, inducing target cell apoptosis, or fix	
CC	complements, where the first protein or peptide molecule is directly	
CC	connected to the second protein or peptide molecule or, optionally, the	
CC	first protein or peptide molecule and the second protein or peptide	
CC	molecule are linked by a third protein or peptide molecule, and where the	
CC	protein molecule is not an antibody, a member of the TNF family or the	
CC	TNF receptor family, and is not conjugated with a bacterial toxin, a	
CC	cytotoxic drug, or a radioisotope), depleting cells in an animal	
CC	(involving administering a modified IgG protein into the blood stream of	
CC	an animal), a polynucleotide that encodes the polypeptide of the	
CC	invention, a cell containing the polynucleotide, a recombinant vector	
CC	capable of expressing the polypeptide, expressing the polypeptide, a	
CC	composition comprising the polypeptide) in combination with one or more	
CC	additional therapeutic compounds, displaying recombinant molecules (which	
CC	molecules include a native or engineered immunoglobulin heavy chain	
CC	variable region, the improvement comprising an immunoglobulin heavy chain	
CC	region that includes one or more mutation, substitution, alteration,	
CC	and/or deletion at one or more amino acid residue corresponding to	
CC	positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable	
CC	region) and a non-naturally occurring single chain antigen-binding	
CC	protein comprising protein having a mutation chosen from a list given in	
CC	the specification. The polypeptides of the invention comprise single	
CC	chain antibodies (scFv, with or without mutated residues) linked via an	
CC	immunoglobulin hinge region (wild-type or mutants where the cysteines are	
CC	changed to serines/prolines and denoted (SSS-P/H, (CSC-S)H etc) to an	
CC	immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which	
CC	may also have mutations in CH2 (e.g. T258N) or a truncated CH3 (e.g. T4	
CC	CH3, a 4 amino acid deletion). The polypeptide may be further linked to a	
CC	non-antibody protein such as the transmembrane and cytoplasmic tail	
CC	(TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are	
CC	useful for neutralization of an infectious agent (where the infectious	
CC	agent is a bacterium, a virus, a parasite, or a fungus) and also for	
CC	treatment of cancer, immune disorders, Grave's disease, Hashimoto's	
CC	disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's	
CC	syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia	
CC	gravis. The present sequence is an antibody peptide or fragment (scFv,	
CC	hinge, CH region, VL or VH) used in a fusion protein of the invention.	
XX	Sequence 331 AA;	
SQ		
Query Match		100.0%; Score 1707; DB 9; Length 331;
Best Local Similarity		100.0%; Pred. No. 4.3e-129;
Matches 320; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	FTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLBDGQVMDVLDLSTASTTQE 60
DB	8	FTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLBDGQVMDVLDLSTASTTQE 67
QY	61	GELASTQSELTLSQKHWSLDRITTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120
DB	68	GELASTQSELTLSQKHWSLDRITTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 127
QY	121	LFIRKSPPTITCLVLDLAPSKGTVNLWTSRASGKPVNHSRKEKQNGTLTVTSTLPVGT 180
DB	128	LFIRKSPPTITCLVLDLAPSKGTVNLWTSRASGKPVNHSRKEKQNGTLTVTSTLPVGT 187

QY 181 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPWPGRSKRKLTLACLIQ 240
 DB 188 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPWPGRSKRKLTLACLIQ 247
 QY 241 NFMPEDISVQWLHNEVQLPDRHSTTPQPRKTKSGGFFVFSRLEVTAEWEQKDFICRAV 300
 DB 248 NFMPEDISVQWLHNEVQLPDRHSTTPQPRKTKSGGFFVFSRLEVTAEWEQKDFICRAV 307
 QY 301 HEAASPSQTVQRAVSNPGK 320
 DB 308 HEAASPSQTVQRAVSNPGK 327
 RESULT 12
 ID ADY21722 standard; protein; 331 AA.
 AC ADY21722;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Human IgE Fc (CH2-CH3-CH4) protein.
 XX
 KW Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;
 KW antibody engineering; cancer; neoplasm; cytostatic; immune disorder;
 KW graves disease; antithyroid; endocrine disease; hashimoto's disease;
 KW immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;
 KW inflammation; musculoskeletal disease; systemic lupus erythematosus;
 KW antinflammatory; dermatological; dermatological disease;
 KW metabolic disorder; sjogrens syndrome; ocular disease;
 KW thrombocytopenic purpura; hemostatic; hematological disease;
 KW multiple sclerosis; neuroprotective; neurological disease;
 KW myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;
 KW fungicide; viral infection; virucide; parasitic infection; antiparasitic;
 KW fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN WO2005017148-A1.
 XX
 PD 24-FEB-2005.
 XX
 PF 24-DEC-2003; 2003WO-US041600.
 XX
 PR 26-JUL-2003; 2003US-00627556.
 XX
 PA (TRUB-) TRIBION PHARM INC.
 XX
 PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 XX
 DR WPI; 2005-182370/19.
 DR N-PSDB; ADY21721.
 XX
 PT New non-naturally occurring single chain protein comprising polypeptides
 PT with binding domain, connecting regions and N-terminally truncated
 PT immunoglobulin, having immunological activity, useful for neutralizing
 PT infectious agent.
 XX
 PS Disclosure; Page 321; 590pp; English.
 XX
 CC The invention relates to a non-naturally occurring single chain protein
 CC (I) comprising a first polypeptide having a binding domain polypeptide
 CC capable of binding to a target molecule, the binding domain polypeptide
 CC comprising a heavy chain variable region, which comprises an amino acid
 CC substitution or deletion at one or more amino acid residues, a second
 CC polypeptide comprising a connecting region attached to the first
 CC polypeptide, and a third polypeptide comprising an N-terminally truncated
 CC immunoglobulin heavy chain constant region polypeptide attached to the
 CC second polypeptide, where the non-naturally occurring single-chain
 CC protein is capable of an immunological activity. Also included are
 CC reducing a target cell population in a subject (involving administering
 CC to the subject a protein that is less than 150 kD, which involves
 CC treating the target cell population with a first protein or peptide that

CC binds to cells within the target cell population, and treating the target
 CC cell population with a second protein or peptide that capable of at least
 CC one of binding an Fc receptor, inducing target cell apoptosis, or fix
 CC complements, where the first protein or peptide molecule is directly
 CC connected to the second protein or peptide molecule or, optionally, the
 CC first protein or peptide molecule and the second protein or peptide
 CC molecule are linked by a third protein or peptide molecule, and where the
 CC protein molecule is not an antibody, a member of the TNF family or the
 CC TNF receptor family, and is not conjugated with a bacterial toxin, a
 CC cytotoxic drug, or a radioisotope), depleting cells in an animal
 CC (involving administering a modified IgE protein into the blood stream of
 CC an animal), a polynucleotide that encodes the polypeptide of the
 CC invention, a cell containing the polynucleotide, a recombinant vector
 CC capable of expressing the polypeptide, expressing the polypeptide, a
 CC composition comprising the polypeptide) in combination with one or more
 CC additional therapeutic compounds, displaying recombinant molecules (which
 CC molecules include a native or engineered immunoglobulin heavy chain
 CC variable region, the improvement comprising an immunoglobulin heavy chain
 CC region that includes one or more mutation, substitution, alteration,
 CC and/or deletion at one or more amino acid residue corresponding to
 CC positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable
 CC region) and a non-naturally occurring single chain antigen-binding
 CC protein comprising protein having a mutation chosen from a list given in
 CC the specification. The polypeptides of the invention comprise single
 CC chain antibodies (scFv, with or without mutated residues) linked via an
 CC immunoglobulin hinge region (wild-type or mutants where the cysteines are
 CC changed to serines/prolines and denoted (SSS-PH, (CSC-S)H etc) to an
 CC immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which
 CC may also have mutations in CH2 (e.g. T256N) or a truncated CH3 (e.g. T4
 CC CH3, a 4 amino acid deletion). The polypeptide may be further linked to a
 CC non-antibody protein such as the transmembrane and cytoplasmic tail
 CC (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are
 CC useful for neutralization of an infectious agent (where the infectious
 CC agent is a bacterium, a virus, a parasite, or a fungus) and also for
 CC treatment of cancer, immune disorders, Grave's disease, Hashimoto's
 CC disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's
 CC syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia
 CC gravis. The present sequence is an antibody peptide or fragment (scFv,
 CC hinge, CH region, VL or VH) used in a fusion protein of the invention.
 XX
 SQ Sequence 331 AA;

Query Match 100.0%; Score 1707; DB 9; Length 331;
 Best Local Similarity 100.0%; Pred. No. 4.3e-129;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDCQVMDVLDLSTASTQOE 60
 DB 8 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDCQVMDVLDLSTASTQOE 67
 QY 61 GELASTQSELTLQKHLSLDRYTCQVYQGHTEPDSKCCADSNPRGVSAYLSRSPFD 120
 DB 68 GELASTQSELTLQKHLSLDRYTCQVYQGHTEPDSKCCADSNPRGVSAYLSRSPFD 127
 QY 121 LFIKSPITICLVVDLAPSKGTVALNTWSRASKPVNHSTRKEEKQNGTLTWTSLPVG 180
 DB 128 LFIKSPITICLVVDLAPSKGTVALNTWSRASKPVNHSTRKEEKQNGTLTWTSLPVG 187
 QY 181 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPWPGRSKRKLTLACLIQ 240
 DB 188 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPWPGRSKRKLTLACLIQ 247
 QY 241 NFMPEDISVQWLHNEVQLPDRHSTTPQPRKTKSGGFFVFSRLEVTAEWEQKDFICRAV 300
 DB 248 NFMPEDISVQWLHNEVQLPDRHSTTPQPRKTKSGGFFVFSRLEVTAEWEQKDFICRAV 307
 QY 301 HEAASPSQTVQRAVSNPGK 320
 DB 308 HEAASPSQTVQRAVSNPGK 327
 RESULT 13
 AAP80291

ID AAP80291 standard; protein; 367 AA.
XX AC AAP80291;
XX DT 25-MAR-2003 (revised)
XX DT 06-DEC-1990 (first entry)
XX DE Interleukin-2/IgE Fc fusion protein.
XX KW Interleukin-2; IgE Fc receptor; fusion protein; asthma; dermatitis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..20
FT Peptide /label= IL-2 leader sequence
FT Peptide 21..31
FT Peptide /label= IL-2 N-terminal
FT Peptide 32..36
FT Peptide /label= linker
FT Peptide 37..367
XX EP269455-A.
XX PN 01-JUN-1988.
XX PD 27-NOV-1987; 87EP-00310475.
XX PF 28-NOV-1986; 86JP-00281871.
XX PR 18-SEP-1987; 87JP-00232295.
XX XX (TAKE) TAKEDA CHEM IND LTD.
XX PI Ikeyama S, Nishimura O;
XX WPI; 1988-149211/22.
XX Fused protein for allergy treatment - comprising interleukin-2 N-terminal
FT residues, a linker and human immunoglobulin E Fc fragment.
XX PS Disclosure; Page ?; 19pp; English.
XX CC This fusion protein has a low toxicity and is useful in therapy for
CC allergy induced by IgE. It can be used in the treatment of allergic
CC dermatosis, atopic dermatitis or bronchial asthma. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX SQ Sequence 367 AA;
Query Match 100.0%; Score 1707; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 4.9e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 60
Db 48 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 107
QY 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db 108 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 167
QY 121 LFIKRSPTITCLVVDLAPSGTGNLTWSRAGRPVNHSTRKEEKQKNGTLTVTSTLPVGT 180
Db 168 LFIKRSPTITCLVVDLAPSGTGNLTWSRAGRPVNHSTRKEEKQKNGTLTVTSTLPVGT 227
QY 181 RDMIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 228 RDMIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 287
QY 241 NFWPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLEVTRAWEQKDEFICRAV 300
Db 288 NFWPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLEVTRAWEQKDEFICRAV 347

QY 301 HEAAPSQTQVRASVNPCK 320
Db 348 HEAAPSQTQVRASVNPCK 367
RESULT 14
AAO19666
ID AAO19666 standard; protein; 427 AA.
XX AC AAO19666;
XX DT 28-MAR-2003 (first entry)
XX DE Human IgE heavy chain constant region.
XX KW Human; IgE; immunoglobulin E; immunotherapy; immune disease;
KW Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.
XX OS Homo sapiens.
XX PN WO200288317-A2.
XX PD 07-NOV-2002.
XX PF 01-MAY-2002; 2002WO-US013527.
XX PR 01-MAY-2001; 2001US-00847208.
XX PR 24-OCT-2001; 2001US-00000439.
XX XX (REGC) UNIV CALIFORNIA.
XX PI Saxon A, Zhang K, Zhu D;
XX WPI; 2003-103456/09.
XX New fusion molecules comprising polypeptide sequences that bind to IgG
FT inhibitory receptor and native IgE receptor, useful for treating IgE-
FT mediated hypersensitivity reactions, e.g. asthma or allergies, or
FT autoimmune diseases.
XX PS Disclosure; Fig 5; 116pp; English.
XX CC The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IgE receptor
CC (FcepsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC treating an IgE-mediated biological response, preferably an IgE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgE
CC heavy chain constant region
XX SQ Sequence 427 AA;
Query Match 100.0%; Score 1707; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 6e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 60
Db 108 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 167
QY 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120

Db 168 GELASTQSELTLSQKHWLSDRYTCQVYQCHTFEDSTKCCADSNPRGVSAYLSRPSFD 227
Qy 121 LFIKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 180
Db 228 LFIKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 287
Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 288 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 347
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDFICRAV 300
Db 348 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDFICRAV 407
Qy 301 HEAASPSQTVQRAVSVNPGK 320
Db 408 HEAASPSQTVQRAVSVNPGK 427

RESULT 15
AAM47863
ID AAM47863 standard; protein; 428 AA.
XX AC AAM47863;
XX AC
DT 22-FEB-2002 (first entry)
XX Human Ig-E heavy chain constant region amino acid sequence.
DE Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
KW transgenic plant.
XX Homo sapiens.
XX WO200183529-A2.
XX 08-NOV-2001.
XX 28-APR-2001; 2001WO-US013932.
XX 28-APR-2000; 2000US-0200298P.
XX (PLAN-) PLANET BIOTECHNOLOGY INC.
XX Larrick JW, Wycoff KL;
XX WPI; 2002-041481/05.
XX N-PSDB; ABA05278.

XX Immunoadhesin for treating human rhinovirus infection comprises chimeric
XX intercellular adhesion molecule-1, and optionally a J chain and secretory
XX component in association.
XX Disclosure; Fig 7; 138pp; English.
XX The invention relates to an immunoadhesin comprising: (a) a chimeric
XX intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor
XX protein linked to at least a portion of an immunoglobulin heavy chain;
XX and (b) optionally a J chain and secretory component associated with the
XX chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
XX glycosylation and virucide activity. The immunoadhesin is useful for
XX reducing infection by human rhinovirus (HRV) and hence the initiation or
XX spread of the common cold by HRV. The immunoadhesin binds to HRV and
XX reduces its infectivity, competing with cell surface ICAM-1 for binding
XX sites, interfering with virus entry or uncoating and directing premature
XX release of viral RNA and formation of empty capsids. Expression of the
XX immunoadhesin in plants would be tetrameric, rather than dimeric.
XX Immunoadhesin having multiple binding sites have a higher effective
XX affinity for the virus, thereby increasing the effectiveness of the
XX immunoadhesin. Association of secretory component and immunoglobulin J
XX chain increases the stability of the immunoadhesin in the mucosal
XX environment. Production is significantly less expensive in plants than in

CC animal cell culture and production in plants is safer for human use,
CC since plants are not known to harbor any animal viruses. The present
CC sequence is that of a human immunoglobulin protein sequence, useful to
CC the invention
XX
SQ Sequence 428 AA;
Query Match 100.0%; Score 1707; DB 5; Length 428;
Best Local Similarity 100.0%; Pred. No. 6e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTPPTVKILOSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTQOE 60
Db 109 FTPPTVKILOSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTQOE 168
Qy 61 GELASTQSELTLSQKHWLSDRYTCQVYQCHTFEDSTKCCADSNPRGVSAYLSRPSFD 120
Db 169 GELASTQSELTLSQKHWLSDRYTCQVYQCHTFEDSTKCCADSNPRGVSAYLSRPSFD 228
Qy 121 LFIKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 180
Db 229 LFIKSPITICLVVDLAPSKGTVNLTWASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 288
Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 289 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 348
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDFICRAV 300
Db 349 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDFICRAV 408
Qy 301 HEAASPSQTVQRAVSVNPGK 320
Db 408 HEAASPSQTVQRAVSVNPGK 428

Search completed: November 30, 2005, 00:51:24
Job time : 154.464 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:46:45 ; Search time 30.1449 Seconds
(without alignment)
1021.378 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVKILQSSCDGGGHFP.....HEAASPSQTVQRAVSVPNGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	428	1 EHHU	Ig epsilon chain C
2	1644.5	96.3	426	2 I36948	Ig epsilon-chain -
3	793	46.5	429	1 EHRT	Ig epsilon chain C
4	751	44.0	388	1 EHMS	Ig epsilon chain C
5	716	41.9	548	2 S38864	Ig epsilon chain C
6	678.5	39.7	423	1 EHMS	Ig epsilon chain C
7	576	33.7	227	2 PH1215	Ig epsilon chain C
8	576	33.7	243	2 PH1216	Ig epsilon chain C
9	570	33.4	115	2 E53116	Ig epsilon chain C
10	471	27.6	572	2 B46529	Ig Y heavy chain (
11	470	27.5	433	2 S31436	Ig epsilon chain -
12	469	27.5	504	2 S00390	Ig gamma chain (cl
13	455.5	26.7	549	2 S04845	Ig heavy chain pre
14	439.5	25.7	455	1 MHMS	Ig mu chain C regi
15	439.5	25.7	455	2 A24976	Ig mu chain C regi
16	433	25.4	328	2 I47158	Ig gamma 1 chain c
17	430.5	25.2	476	1 MHMS	Ig mu chain C regi
18	428.5	25.1	454	1 MHY	Ig mu chain C regi
19	428	25.1	328	2 I47161	Ig gamma 3 chain c
20	416	24.4	326	1 G2HU	Ig gamma-2 chain C
21	415	24.3	328	2 I47159	Ig gamma 2a chain
22	414	24.3	444	2 PC4436	monoclonal antibod
23	413.5	24.2	457	2 S03961	Ig mu chain C regi
24	413	24.2	453	2 S37768	Ig mu chain C regi
25	412	24.1	328	2 I47160	Ig gamma 2b chain
26	411.5	24.1	470	2 S22080	Ig heavy chain pre
27	410	24.0	391	1 MHUBT	Ig mu heavy chain
28	409.5	24.0	343	2 S25644	Ig mu chain C regi
29	409	24.0	592	2 S25705	Ig mu chain - shee

Ig mu chain C regi
Ig gamma-2 chain C
Ig heavy chain - h
Ig mu chain C regi
Ig gamma-1 chain C
Ig gamma 4 chain c
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-1 chain C
Ig gamma-1 chain C
Ig mu chain C regi
Ig mu chain precu
Ig gamma-2b chain
Ig gamma-1 chain -
Ig gamma-2a chain

ALIGNMENTS

RESULT 1

EHHU

Ig epsilon chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence Revision 13-Jun-1983 #text Change 09-Jul-2004

C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46

R:Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene

A:Reference number: A22771; MUID:84236029; PMID:6234164

A:Accession: A22771

A:Molecule type: DNA

A:Residues: 1-428 <FLA>

A:CROSS-references: UNIPROT:P01854; UNIPARC:UPI000004BB48; GB:I00022; GB:J00227; GB:V005

R:Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog

A:Reference number: A23195; MUID:84207910; PMID:6327276

A:Accession: A23195

A:Molecule type: DNA

A:Residues: 2-428 <UED>

A:CROSS-references: UNIPARC:UPI0000173783; GB:J00222; NID:g184755

R:Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992

A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing

A:Reference number: PH1214; MUID:92308839; PMID:1613458

A:Accession: PH1214

A:Molecule type: DNA

A:Residues: 320-428 <ZHA>

A:CROSS-references: UNIPARC:UPI000014452D; EMBL:X63693; GB:S38668; NID:g32987

R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasaki, R.; Igarashi, K.; Kikuchi, M.; Sug

Nucleic Acids Res. 11, 719-726, 1983

A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon ch

A:Reference number: A93491; MUID:83168897; PMID:6300763

A:Accession: A93491

A:Molecule type: mRNA

A:Residues: 1-428 <SEN>

A:CROSS-references: UNIPARC:UPI000004BB48; GB:I00022; GB:J00227; GB:V00555; NID:g185035

R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.

Cell 29, 691-699, 1982

A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.

A:Reference number: A90824; MUID:83001945; PMID:6288268

A:Accession: A90824

A:Molecule type: DNA

A:Residues: 1-358,'L',360-428 <MAX>

A:CROSS-references: UNIPARC:UPI0000173784; GB:J00222; NID:g184755

A:Note: this sequence difference may be due to polymorphism

R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-1

A:Reference number: A94418

A:Accession: A94418

A:Molecule type: protein

A:Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',99-121,'B',99-121,'B',99-121,'B',99-121,'L',111
A:Cross-references: UNIPARC:UPI00000173785
A:Experimental source: myeloma protein Nd
R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; C
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A>Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: B93933
A:Molecule type: mRNA
A:Residues: 1-40;68-114;427-428 <KEN>
A:Cross-references: UNIPARC:UPI00001592FD; UNIPARC:UPI0000173786; UNIPARC:UPI00000173787;
R:Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A>Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
A:Reference number: S02438; MUID:88083554; PMID:3121387
A:Accession: S02438
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 98-352 <IKE>
A:Cross-references: UNIPARC:UPI0000173788
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A>Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: A53116
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 320-428 <ZH2>
A:Cross-references: UNIPARC:UPI000014452D
A:Experimental source: myeloma U266-derived cell line AF-10
A>Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R:Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A>Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A:Reference number: A46336; MUID:93122085; PMID:8419166
A:Accession: A46336
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-426 <HEL>
A:Cross-references: UNIPARC:UPI0000113EF7; GB:S55273; NID:G263166; PIDN:AAB24857.1; PID:
A:Experimental source: B cell myeloma U-266
A>Note: sequence extracted from NCBI backbone (NCBIP:125297)
A:Accession: A46336
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-391 <HE2>
A:Cross-references: UNIPARC:UPI0000113EP8; GB:S55276; NID:G263168; PIDN:AAB24858.1; PID:
A:Experimental source: B cell myeloma U-266
A>Note: sequence extracted from NCBI backbone (NCBIP:125299)
A:Accession: A46336
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: UNIPARC:UPI0000113EP5; GB:S53497; NID:G263162; PIDN:AAB24855.1; PID:
A:Experimental source: B cell myeloma U-266
A>Note: sequence extracted from NCBI backbone (NCBIP:123483)
C:Genetics:
A:Gene: GDB:IGHE
A:Cross-references: GDB:119335; OMIM:147180
A:Map position: 14q32.33-14q32.33
A:Introns: 1/1; 104/1; 211/1; 319/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (<kappa>
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:22-87/Domain: immunoglobulin homology <IMI>
F:128-195/Domain: immunoglobulin homology <IM2>
F:232-301/Domain: immunoglobulin homology <IM3>
F:338-407/Domain: immunoglobulin homology <IM4>
F:14/Disulfide bonds: interchain (to light chain) #status predicted
F:15-105,29-85,135-193,239-299,345-405/Dissulfide bonds: #status predicted
F:21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:121,209/Dissulfide bonds: interchain (to heavy chain) #status predicted

```

Query Match      100.0%; Score 1707; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 2.2e-119;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  FTPPTVKILOSSCDGGGHFFPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTASTQOE 60
Db      109  FTPPTVKILOSSCDGGGHFFPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTASTQOE 168
QY      61  GELASTQSELTLSQKHWSLDRTYTCQVTYQCHTFEDSTKKCADSPNPGVSAVLSRPSFPD 120
Db      169  GELASTQSELTLSQKHWSLDRTYTCQVTYQCHTFEDSTKKCADSPNPGVSAVLSRPSFPD 228
QY      121  LFRKSTPTIICLVLDLAPSGKTWNLTWSRAGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 180
Db      229  LFRKSTPTIICLVLDLAPSGKTWNLTWSRAGKPVNHSTRKEEKQRNGTLTVTSTLPVGT 288
QY      181  RDMTEGTYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIO 240
Db      289  RDMTEGTYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIO 348
QY      241  NFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLEVTVAEWSQKDFICRAV 300
Db      349  NFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLEVTVAEWSQKDFICRAV 408
QY      301  HEAASPSQTVQRAVSVNPGK 320
Db      409  HEAASPSQTVQRAVSVNPGK 428

RESULT 2
I36948
lg epsilon-chain - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: I36948
R:Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and
A:Reference number: I36948; MUID:87147196; PMID:3103123
A:Accession: I36948
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <RES>
A:Cross-references: UNIPARC:UPI0000117548; GB:M15398; NID:gl76797; PIDN:AAA3541
C:Genetics:
A:Introns: 103/1; 209/1; 317/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:336-405/Domain: immunoglobulin homology <IMM>

```

2

Db	238	FPKPKDVLTRSTLIQYCFYGHILNDVSVSWLMDREITDTTLAQTVLKEEGKLASTCS	297
Qy	69	ELTUSQHWLSDRYTCQVYQGHTFEDSTKCCADSNRGSAYLSRSPFDJLFIKSPPT	128
Db	298	KLNIITEQQWMSSEFTCKVTSQGVLYLAHTRRCPDHEPRGVITYLIPPSPLDLYQNGAPK	357
Qy	129	ITCLVVDLAPSKGVNLTWSRASGKPNVHSTRKEEKORNGTLTVTSTLPVGTDRDWIETG	188
Db	358	LTCLVVDLESEK-NVNVWVWQEKTSVSASQWYTKHNNATTSTISLTPVAKDWIEGYG	416
Qy	189	YQCRVTHPHLPRLMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIONFMPEDIS	248
Db	417	YQCVVDHDPFKPIVRITKTPGORSAPENVVPPPE-EESEDKRTLCLIQNFPPEDIS	475
Qy	249	YQWLHNEVQLPDARHSTTOPRKTGKS--GFFVFSRLVETRAEWQKDEFICRAVHEAASP	306
Db	476	VQWLGDGKLINSQHSSTTTLKSGNSNRGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQK	535
Qy	307	SQTVQRAVSVN	317
Db	536	PRKLEKTISTS	546
RESULT 6			
EHMSS			
Ig epsilon chain C region (version 2) - mouse			
C/Species: Mus musculus (house mouse)			
C/Date: 30-Jun-1997 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004			
C/Accession: A02145			
R/Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.			
EMBO J. 1, 1117-1123, 1982			
A/Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with human epsilon gene			
A/Reference number: A90966; MUID:84236092; PMID:6329728			
A/Accession: A02145			
A/Molecule type: DNA			
A/Residues: 1-423 <IGH>			
A/Cross-references: UNIPROT:P06336; UNIPARC:UPI000017378A			
A/Note: the sequence was determined from the germline gene			
C/Genetics:			
A/Introns: 91/1; 199/1; 307/1			
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger aggregates.			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin			
F/16-77/Domain: immunoglobulin homology <IMM1>			
F/115-183/Domain: immunoglobulin homology <IMM2>			
F/220-288/Domain: immunoglobulin homology <IMM3>			
F/325-396/Domain: immunoglobulin homology <IMM4>			
F/23-75,122-181,227-286,332-394/Disulfide bonds: #status predicted			
F/43,84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 39.7%; Score 678.5; DB 1; Length 423;			
Best Local Similarity 43.7%; Pred. No. 5.5e-43;			
Matches 136; Conservative 56; Mismatches 112; Indels 7; Gaps 6;			
Qy	13	CDGGGHPPIQLCLVSGYTPGTINTWL-EGQVMDVDLSTASTTQBELASTQSELT	71
Db	109	CDPNA-FHSTLIQYCFYGHILNDVSVSWLMDREITDTTLAQTVLKEEGKLASTCSKLN	167
Qy	72	LSQKHWLSDRYTCQVYQGHTFEDSTKCCADSNRGSAYLSRSPFDLFIKSPPTIC	131
Db	168	ITFQQWMSSEFTCRVTSQGVLYLAHTRRCPDHEPRGVITYLIPPSPLDLYQNGAPKLT	227
Qy	132	LVDLAPSKGVNLTWSRASGKPNVHSTRKEEKORNGTLTVTSTLPVGTDRDWIEGTYQC	191
Db	228	LVDLESEK-NVNVWVWQEKTSVSASQWYTKHNNATTSTISLTPVAKDWIEGYGYQC	286
Qy	192	RVTHPHLPRLMRSTTKTS-GPRAAPEVYAFATPEWPGSRDKRTLACLIONFMPEDISVQ	250
Db	287	VDRPDPFKPIVRISITLIPQVRSQSAPEVYVPPPE-EESEDKRTLCLIQNFPPEDISVQ	345
Qy	251	WLHNEVQLPDARHSTTOPRKTGKS--GFFVFSRLVETRAEWQKDEFICRAVHEAASPQ	308

Db	346	WLGDGKLINSQHSSTTTLKSGNSNRGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPR	405
Qy	309	TVORAVSVNPG	319
Db	406	KLEKTISTSIG	416
RESULT 7			
PHI215			
Ig epsilon chain C region form 2 - human (fragment)			
C/Species: Homo sapiens (man)			
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000			
C/Accession: PHI215			
R/Zhang, K.; Saxon, A.; Max, E.E.			
J. Exp. Med. 176, 233-243, 1992			
A/Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing			
A/Reference number: PHI214; MUID:92308839; PMID:1613458			
A/Accession: PHI215			
A/Molecule type: DNA			
A/Residues: 1-227 <ZHA>			
A/Cross-references: UNIPARC:UPI0000176EFC; EMBL:X63693			
C/Genetics:			
A/Introns: 108/1; 200/3			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: alternative splicing; immunoglobulin			
F/19-88/Domain: immunoglobulin homology <IMM>			
Query Match 33.7%; Score 576; DB 2; Length 227;			
Best Local Similarity 100.0%; Pred. No. 1.1e-35;			
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	212	PRAAPEVYAFATPEWPGSRDKRTLACLIONFMPEDISVQWLHNEVQLPDARHSTTOPRKT	271
Db	1	PRAAPEVYAFATPEWPGSRDKRTLACLIONFMPEDISVQWLHNEVQLPDARHSTTOPRKT	60
Qy	272	KSGGFFVFSRLVETRAEWQKDEFICRAVHEAASPSQTVORAVSVNPG	319
Db	61	KSGGFFVFSRLVETRAEWQKDEFICRAVHEAASPSQTVORAVSVNPG	108
RESULT 8			
PHI216			
Ig epsilon chain C region form 3 - human (fragment)			
N/Alternate names: Ig epsilon chain C region, membrane-bound form (clone CH4-M2')			
C/Species: Homo sapiens (man)			
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000			
C/Accession: PHI216; D53116			
R/Zhang, K.; Saxon, A.; Max, E.E.			
J. Exp. Med. 176, 233-243, 1992			
A/Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing			
A/Reference number: PHI214; MUID:92308839; PMID:1613458			
A/Accession: PHI216			
A/Molecule type: DNA			
A/Residues: 1-243 <ZHA>			
A/Cross-references: UNIPARC:UPI0000176EFD; EMBL:X63693			
R/Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.			
J. Biol. Chem. 269, 456-462, 1994			
A/Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces			
A/Reference number: A53116; MUID:94103254; PMID:8276835			
A/Accession: D53116			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-243 <ZH2>			
A/Cross-references: UNIPARC:UPI0000176EFD			
A/Experimental source: myeloma U266-derived cell line AF-10			
A/Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIN:141711, NCBIN:141718)			
C/Genetics:			
A/Introns: 108/1			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: alternative splicing; immunoglobulin			
F/19-88/Domain: immunoglobulin homology <IMM>			
Query Match 33.7%; Score 576; DB 2; Length 243;			

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Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 212 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 271
Db 1 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 60

Qy 272 KSGGFFVFSRLVTRAEWEQDEFCICRAVHEAASPSQTVQRAVSNPG 319
Db 61 KSGGFFVFSRLVTRAEWEQDEFCICRAVHEAASPSQTVQRAVSNPG 108

RESULT 9
E53116
Ig epsilon chain C region, secreted splice form (clone CH4-3'UT-CH5-M2'') - human (fragm
C:Species: Homo sapiens (man)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: E53116
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: E53116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <ZRA>
A:Cross-references: UNIPARC:UPI0000176EFF
A:Experimental source: Myeloma U266-derived cell line AP-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141720)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 33.4%; Score 570; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 212 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 271
Db 1 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 60

Qy 272 KSGGFFVFSRLVTRAEWEQDEFCICRAVHEAASPSQTVQRAVSNP 318
Db 61 KSGGFFVFSRLVTRAEWEQDEFCICRAVHEAASPSQTVQRAVSNP 107

RESULT 10
B46529
Ig Y heavy chain (7.8S) - duck
N:Alternate names: Ig gamma chain (7.8S)
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A:Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: m
A:Reference number: A46529; MUID:93017865; PMID:1401901
A:Accession: B46529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAG>
A:Cross-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:G62442; PIDN:CAA46322.1; PII
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIP:116127)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 27.6%; Score 471; DB 2; Length 572;
Best Local Similarity 32.0%; Pred. No. 2e-27;
Matches 106; Conservative 66; Mismatches 141; Indels 18; Gaps 10;

Qy 2 TPPTVKILOSS-CDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLSASTTQE 60
```

```
Db 248 TPPEVQLHSSVCSTLG--DDSVELLCVITGFSPPPVEVWLDG--APAHLVATMRPQ 303
Qy 61 GELAS-----TQSELTLSQKWLSDRYTTCQVY--QGHTEFSTKKCADSNPRG---VSA 111
Db 304 REAGSKTYMATSQTNVSREDWKAGKAFCTCRVHPATGCTAGHARFCGSGAQCSCSIQI 363
Qy 112 YLSRSPFDLFIKSPPTITCLVVVDLAPSKGTVNLTWSRASGKPVNHSRTRKEEKORNGTLT 171
Db 364 FVPPSPGSLYIQDAKVHCLVNL-PSDASLSISWTREKSGALRPDPMLTEHFNGTFT 422
Qy 172 VTSLPVGTRDWIEGYQCRVTHPHLPALRMSTTTKSGPRAAPEYAFATPEWPGSRD 231
Db 423 ASSSLAISTQDLAGERFTCTVQHEDLPVPLGKSIAGKAGKVATPYITFTPPHAEELSLSA 482
Qy 232 KRLIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT--RKTGSG-FEVSRLVTRAEW 289
Db 483 EVTLTCLVIRGQFQPEVQWLRNHSVPAAEFVTPPLKBPNGDGTFFLYSKMTVPKASW 542
Qy 290 EOKDEFICRAVHEAASPSQTVQRAVSNPGK 320
Db 543 QGGVSYACMVVHEGL-PWRFTQRPLOKTPGK 572

RESULT 11
S31436
Ig upsilon chain - axolotl (fragment)
C:Species: Ambystoma mexicanum (axolotl)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C:Accession: S31436
R:Fellah, J.S.; Wiles, M.V.; Schwager, J.; Charlemagne, J.
submitted to the EMBL Data Library, November 1992
A:Description: cDNA sequence of Ambystoma mexicanum upsilon heavy Igy chain.
A:Reference number: S31436
A:Accession: S31436
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-433 <FEL>
A:Cross-references: UNIPARC:UPI0000116C7E; EMBL:X69492; NID:G62420; PID:G62421
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 27.5%; Score 470; DB 2; Length 433;
Best Local Similarity 31.0%; Pred. No. 1.7e-27;
Matches 102; Conservative 72; Mismatches 137; Indels 18; Gaps 9;

Qy 4 PTVKILQSSC---DGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLSASTTQE 60
Db 111 PSVQVLOSSCADTDGNG---SIELVCLISGYTPDNIQVRLVNDKMAPIQGQTSPPQKD 166
Qy 61 GE-LASTQSELTLSQKWLSDRYTTCQVYQGHY--PEDSTKKCADS-NPRGVSAVLSRP 116
Db 167 QGGTFTTSQINVTKSDWASGDKTCKVEHPATSRADTTIHNCADSTQTPQPKVFLAP 226
Qy 117 SPFDLFIKSPPTITCLVVVDLAPSKGTVNLTWSRASGKPVNHSRTRKEEKORNGTLTSTL 176
Db 227 KARDLYIANQPVVICKITKMSNS-DSLSTVTKRREGPEAAVISEQYIDSDGTFTAMSVL 285
Qy 177 PVGTRDWIEGYQCRVTHPHLPALRMSTTTKSGPRAAPEYAFATPEWPGSRDKRTL 235
Db 286 NITKNEWERGDEFTCKVKHFDLPFPFLSRVSKPTGRSPFAPTPMYPAPHEMELANYDFVSL 345
Qy 236 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSG---FFVFSRLVTRAEWEQ 291
Db 346 TCLVKFSFSPDDIYIQWKQKGVISDKVSNVEPQEQAGTAGLGYFSYSMLTIQKSDWDK 405
Qy 292 KDEFICRAVHEAASPSQTVQRAVSNPGK 320
Db 406 RETFTCYAHSV-PKNLMTERRIQKPLGK 433

RESULT 12
S00390
Ig gamma chain (clone 36) - chicken (fragment)
```


A;Cross-references: UNIPARC:UPI00001737BB
C;Genetics:
A;Introns: 1/1; 106/1; 219/1; 325/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-91/Domain: immunoglobulin homology <IMM1>
F;129-201/Domain: immunoglobulin homology <IMM2>
F;239-307/Domain: immunoglobulin homology <IMM3>
F;346-417/Domain: immunoglobulin homology <IMM4>
F;436-455/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-89/Disulfide bonds: #status experimental
F;46,211,243,281,442/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;136-199,246-305,353-415/Disulfide bonds: #status predicted
F;216,454/Disulfide bonds: interchain (to heavy chain) #status predicted
F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 25.7%; Score 439.5; DB 1; Length 455;
Best Local Similarity 32.3%; Pred. No. 3.4e-25; Mismatches 152; Indels 13; Gaps 8;
Matches 106; Conservative 57;

QY 4 PTVKILQSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQGE 62
DB 112 PNVNVFVPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKGKLVESGFTTDPVTIENK 171

QY 63 LASTQ-----SELTLSQKHWLSDRYTCQVYQGHFT-EDSTKKCADSNPRGVSAYLRSR 116
DB 172 GSTPQYKVIISTLTISEIDWLNLVYTCRDVHRGLTFLKNVSSSTCAASPSTDLTFTIPP 231

QY 117 SPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKQNGTLTSTL 176
DB 232 SFADIFLSKSNLTLCLVSNLATYE-TLNIWASQSGEPLTKIKIMESHHPNGTFSAGVA 290

QY 177 PVGTRDIWIEGTQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATP--EWPGRDKRT 234
DB 291 SVCVEDWNRKEFVCTVTHRDLPSPQKFKISKPNEVHKHPPAVYLLPPAREQLNRESAT 350

QY 235 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGS-GF-FVFSRLLEVTRAWEQK 292
DB 351 VTCLVKGFSPADISVQWLQGLLPQEKYVTSAPMPFGAPGFYTHSILITVTEEMNSG 410

QY 293 DEFICRAVHEAASPSQTQVRAVSNPGK 320
DB 411 ETYTCVVGHEAL-PHLVTERTVDKSTGK 437

RESULT 15
A24976
Ig mu chain C region (allele b) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C;Accession: A24976
R;Schreier, P.H.; Quester, S.; Rothwell, A.
Nucleic Acids Res. 14, 2381-2389, 1986
A;Title: Allotypic differences in murine mu-genes.
A;Reference number: A24976; MUID:86176735; PMID:3083402
A;Accession: A24976
A;Molecule type: mRNA
A;Residues: 1-455 <SCH>
A;Cross-references: UNIPARC:UPI0000115D47; GB:X03690; NID:952381; PIDN:CAA27326.1; PID:9
A;Experimental source: strain C57BL/6
A;Note: the authors translated the codon AAG for residue 65 as Leu
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;346-417/Domain: immunoglobulin homology <IMM>

Query Match 25.7%; Score 439.5; DB 2; Length 455;
Best Local Similarity 32.3%; Pred. No. 3.4e-25; Mismatches 152; Indels 13; Gaps 8;
Matches 106; Conservative 57;

QY 4 PTVKILQSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQGE 62

Search completed: November 30, 2005, 01:11:22
Job time : 31.1449 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:43:39 ; Search time 176.232 Seconds
(without alignments)
1281.091 Million cell updates/sec

Title: US-09-847-208B-6
Perfect score: 1707
Sequence: 1 FTPTVKILQSSCDGGGHP.....HEAASPSQTVQRAVSNVPGK 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707	100.0	428	1 IGHE_HUMAN	P01854 homo sapien
2	793	46.5	429	1 IGHE_RAT	P01855 rattus norv
3	751	44.0	421	1 IGHE_MOUSE	P06336 mus musculu
4	459.5	26.9	560	2 Q4V801_XENLA	Q4V801 xenopus lae
5	448.5	26.3	337	2 Q95M34_HORSE	Q95M34 equus cabal
6	439.5	25.7	454	1 MUC_MOUSE	P01872 mus musculu
7	439.5	25.7	590	2 Q4V9V8_MOUSE	Q4V9V8 mus musculu
8	434.5	25.5	617	2 Q4KML5_MOUSE	Q4KML5 mus musculu
9	431.5	25.3	614	2 Q7TMT6_MOUSE	Q7TMT6 mus musculu
10	430.5	25.2	475	1 MUC_MOUSE	P01873 mus musculu
11	430.5	25.2	613	2 Q8VCX7_MOUSE	Q8VCX7 mus musculu
12	430.5	25.2	616	2 Q504M7_MOUSE	Q504M7 mus musculu
13	426	25.0	464	2 Q6MZU6_HUMAN	Q6MZU6 homo sapien
14	423.5	24.8	454	1 MUC_MESAU	P06337 mesocricetu
15	421	24.7	465	2 Q6P6CA_HUMAN	Q6P6CA homo sapien
16	420	24.6	417	2 Q6N093_HUMAN	Q6N093 homo sapien
17	417	24.4	470	2 Q68CN4_HUMAN	Q68CN4 homo sapien
18	416	24.4	326	1 IGHG2_HUMAN	P01859 homo sapien
19	414	24.3	458	2 Q65ZQ1_HUMAN	Q65ZQ1 homo sapien
20	413.5	24.2	457	1 MUC_SUNMU	P20768 suncus muri
21	413	24.2	375	2 Q86TT1_HUMAN	Q86TT1 homo sapien
22	413	24.2	463	2 Q99LC4_MOUSE	Q99LC4 mus musculu
23	413	24.2	597	2 Q9BU10_HUMAN	Q9BU10 homo sapien
24	413	24.2	597	2 Q9BQB8_HUMAN	Q9BQB8 homo sapien
25	413	24.2	597	2 Q96BB9_HUMAN	Q96BB9 homo sapien
26	413	24.2	597	2 Q6GMX5_HUMAN	Q6GMX5 homo sapien
27	413	24.2	606	2 Q6GMY2_HUMAN	Q6GMY2 homo sapien
28	410.5	24.0	371	2 Q5RK07_RAT	Q5RK07 rattus norv
29	410.5	24.0	590	2 Q569B8_RAT	Q569B8 rattus norv
30	410.5	24.0	591	2 Q510L9_RAT	Q510L9 rattus norv
31	410.5	24.0	591	2 Q4QWQ0_RAT	Q4QWQ0 rattus norv

ALIGNMENTS									
RESULT 1									
IGHE_HUMAN	410.5	24.0	598	2	Q568Y0_RAT	0568y0	rattus norv		
ID_IGHE_HUMAN									
AC	P01854;		391	1	MUCB_HUMAN	P04220	homo sapien		
DT	21-JUL-1986 (Rel. 01, Created)		454	1	MUC_HUMAN	P01871	homo sapien		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		458	1	MUC_RABIT	P03988	oryctolagus		
DT	10-MAY-2005 (Rel. 47, Last annotation update)		329	1	IGHG2_CAVPO	P01862	cavia porce		
DE	Ig epsilon chain C region.		329	1	IGHG2_CAVPO	Q6PF95	mus musculu		
GN	Name=IGHE;		464	2	Q6PF95_MOUSE	Q6N089	homo sapien		
OS	Homo sapiens (Human).		472	2	Q6N089_HUMAN	Q8WUX4	homo sapien		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		595	2	Q8WUX4_HUMAN	Q8WUX4	homo sapien		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		613	2	Q8WUK1_HUMAN	Q8WUK1	homo sapien		
OC	Homo.		620	2	Q96EY0_HUMAN	Q96EY0	homo sapien		
OX	NCBI_TaxID=9606;		625	2	Q96EY0_HUMAN	Q96EY0	homo sapien		
NP	NUCLEOTIDE SEQUENCE.		625	2	Q96EY0_HUMAN	Q96EY0	homo sapien		
RP	MEDLINE=83168897; PubMed=6300763;		324	1	IGHG1_MOUSE	P01868	mus musculu		
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,		464	2	Q6PJP8_MOUSE	Q6PJP8	mus musculu		
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;		465	2	Q6PJP8_MOUSE	Q6PJP8	mus musculu		
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin								
RT	epsilon chain cDNA.";								
RL	Nucleic Acids Res. 11:719-726 (1983).								
RN	[2]								
RP	NUCLEOTIDE SEQUENCE, AND VARIANT LEU-359.								
RP	MEDLINE=83001945; PubMed=6288268; DOI=10.1016/0092-8674(82)90185-4;								
RA	Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;								
RT	"Duplication and deletion in the human immunoglobulin epsilon genes.";								
RL	Cell 29:691-699 (1982).								
RN	[3]								
RP	NUCLEOTIDE SEQUENCE.								
RP	MEDLINE=84236029; PubMed=6234164;								
RA	Flanagan J.G., Rabbitts T.H.;								
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant								
RT	region gene, and evidence for three non-allelic genes.";								
RL	EMBO J. 1:655-660 (1982).								
RN	[4]								
RP	NUCLEOTIDE SEQUENCE.								
RP	MEDLINE=84207910; PubMed=6327276;								
RA	Ueda S., Nakai S., Nishida Y., Hiseajima H., Honjo T.;								
RT	"Long terminal repeat-like elements flank a human immunoglobulin								
RT	epsilon pseudogene that lacks introns.";								
RL	EMBO J. 1:1539-1544 (1982).								
RN	[5]								
RP	PRELIMINARY PROTEIN SEQUENCE (MYELOMA PROTEIN ND).								
RP	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;								
RA	(In) Bach M.K. (eds.);								
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,								
RL	Marcel Dekker, New York (1978).								
RN	[6]								
RP	NUCLEOTIDE SEQUENCE OF 1-40; 68-114 AND 427-428.								
RP	MEDLINE=83065234; PubMed=6815856;								
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,								
RA	Bell L.O., Gould H.J.;								
RT	"Cloning and sequence determination of the gene for the human								

NCBI_TaxID=10116;
[1]
RN NUCLEOTIDE SEQUENCE (IMMUNOCYTOMA IR2).
RC STRAIN=LOU/C/WSL;
RA MEDLINE=83064537; PubMed=6292865;
RX Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
E.";
RL Nucleic Acids Res. 10:6041-6049(1982).
[2]
RN NUCLEOTIDE SEQUENCE OF 168-342 (MYELOMA IR162).
RX MEDLINE=83182019; PubMed=6820340;
RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
RT construction, identification, and DNA sequence.";
RL DNA 1:335-343(1982).
[3]
RN NUCLEOTIDE SEQUENCE OF 205-306.
RX MEDLINE=82174576; PubMed=6803238;
RA Hellman L., Pettersson U., Bennich H.;
RT "Characterization and molecular cloning of the mRNA for the heavy
RT (epsilon) chain of rat immunoglobulin E.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
CC -!- SIMILARITY: Contains 4 Ig-like (immunoglobulin-like) domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; J00744; AAA41379.1; ALT_INIT; mRNA.
DR PIR; A93442; EHRT.
DR HSSP; P01854; 1FP5.
DR Ensembl; ENSRNOG0000005328; Rattus norvegicus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; CI-set; 2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT DOMAIN 6 89
FT Ig-like 1.
FT DOMAIN 103 201
FT Ig-like 2.
FT DOMAIN 205 305
FT Ig-like 3.
FT DOMAIN 314 414
FT Ig-like 4.
FT R -> N (in Ref. 2).
FT CONFLICT 168 168
FT P -> L (in Ref. 2).
FT NON_TER 1
FT SEQUENCE 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;
SQ
Query Match 46.5%; Score 793; DB 1; Length 429;
Best Local Similarity 47.4%; Pred. No. 3,7e-55;
Matches 152; Conservative 54; Mismatches 109; Indels 6; Gaps 5;
QY 2 TPPTVKILQSSCDGGHPPTIQLCLVSGYTPGTINITWL-EDGQVMDVLSLSTATTQ 60
DB 101 TKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHQNDVSIHLMDDRKIVETHAQNVLKEE 159
QY 61 GELASTQSELTISQKHLSDRYTQVYQGHFTFEDSTKCKADSNPRGVSAYLSRPSPD 120
DB 160 GKLASTYSRLNITQQQWMSSESTFTCKVTSQGENYWAHTRCRSDDEPRGVTILIPSPLD 219
QY 121 LFIRKSPITCLVVDLAPSKGTVNLTWASRASKPVNHSRKEEKQNGTLTWTSTLPVGT 180
DB 220 LYENGTFKULCLVLDL-ESEENITVTVRERKKSIGSASQRTKHNATTSISLIPVDA 278
QY 181 RWIEGEGYQCRVTHPLMRSTTKTSGPRAAPVYAFATPWPGRDKRTLCLIQ 240
DB 279 KOWIEGEGYQCRVTHPLMRSTTKTSGPRAAPVYAFATPWPGRDKRTLCLIQ 337

QY 241 NFMPEDISVQWLHNEVQLPDARHSTTPQPRKTKSG--FFVFSRLVETRAWEQKDEFTCR 298
DB 338 NFFPEDISVQWLQDSKLIPKSHSTTTPLKYNQSNORFFFSRLVETKALMTQTKQFTCR 397
QY 299 AVHEAASPSQTVORAVSNVFG 319
DB 398 VIHEALREPRKLERTISKSLG 418
RESULT 3
IGHE MOUSE STANDARD; PRT; 421 AA.
ID IGHE_MOUSE
AC P06336; P01856;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RT comparison with the human epsilon gene sequence.";
RL EMBO J. 1:1117-1123(1982).
[2]
RN SEQUENCE REVISION.
RP Honjo T.;
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE OF 34-421.
RX MEDLINE=8311774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain
RT cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X01857; CAA25977.1; -; Genomic_DNA.
DR EMBL; X01857; CAA25978.1; -; Genomic_DNA.
DR PIR; A02144; EHMS.
DR PIR; A02145; EHMS.
DR HSSP; P01854; 1FP5.
DR Ensembl; ENSMUSG000000021153; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
FT REGION 1 90
FT CH1.
FT REGION 91 197
FT CH2.
FT REGION 198 304
FT CH3.
FT REGION 305 421
FT CH4.
FT N-linked (GlcNAc...) (Potential).
FT CARBOHYD 43 43
FT N-linked (GlcNAc...) (Potential).
FT CARBOHYD 72 72
FT N-linked (GlcNAc...) (Potential).
FT CARBOHYD 84 84
FT N-linked (GlcNAc...) (Potential).
FT CARBOHYD 95 95
FT N-linked (GlcNAc...) (Potential).
FT CARBOHYD 166 166
FT N-linked (GlcNAc...) (Potential).
FT CARBOHYD 238 238
FT N-linked (GlcNAc...) (Potential).
FT CARBOHYD 261 261
FT N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 365 365 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 415 415 N-linked (GlcNAc... ) (Potential).
FT DISULFID 23 75 By similarity.
FT DISULFID 121 180 By similarity.
FT DISULFID 226 285 By similarity.
FT DISULFID 330 392 By similarity.
FT NON TER 1 1
SQ SEQUENCE 421 AA; 47321 MW; 8F909E1F30A06B47 CRC64;

Query Match 44.0%; Score 751; DB 1; Length 421;
Best Local Similarity 45.8%; Pred. No. 8.6e-52;
Matches 147; Conservative 59; Mismatches 109; Indels 6; Gaps 5;

QY 2 TPTVKILQSCDGGHPPTIQLLCLVSGYTGTTNITWL-EDGQVMDVLDSTASTQGE 60
DB 97 TEPTLELLHSSCDFNA-FHSTIQLYCFIYGHILNDVSVSLWMDREITDTLAQTVLKKE 155
QY 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHFTFEDSTKCCADSPRGVSAYLSRPSFD 120
DB 156 GKLASTCSKLNITEQQWMSSTFTCKVTSQVDYLAHTRCPDHEPRGVITYLIPSPLD 215
QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWRSAGKPVNHSTRKEBKORNGTLTVTSTLPVGT 180
DB 216 LYQNGAPKLCVLVDLESER-NNVNTWNEKKTSSVSASQWYTKHNNATTSTSLPVVA 274
QY 181 RDWIEGTQYQVRVTHPHLPALMRSTTKTGSPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
DB 275 KDWIEGYGYCIVDHPDPFPKPIVRSITKTPQRSAPENVYVFPFPE-EESDKRTLCLIQ 333
QY 241 NFWPDISVQWLHNEVOLPDARHSTTQPRKTGS--GFFVFSRLVETRAEWEQKDSFICR 298
DB 334 NFPEDISVQWLHNEVOLPDARHSTTQPRKTGS--GFFVFSRLVETRAEWEQKDSFICR 298
QY 299 AVHEAASPSQTVQRAVSNVPG 319
DB 394 VIHEALQKPRKLEKTISTSLG 414

RESULT 4
Q4V801 XENLA PRELIMINARY; PRT; 560 AA.
AC Q4V801;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE LOC398774 protein.
GN Names=LOC398774;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Siemen C.M., Schuler G.D.,
RA Atlshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
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RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC097629; AAH97629.1; -, mRNA.
SQ SEQUENCE 560 AA; 61795 MW; 9DED2DD2B17CFDBE CRC64;

Query Match 26.9%; Score 459.5; DB 2; Length 560;
Best Local Similarity 33.1%; Pred. No. 3.2e-28;
Matches 107; Conservative 60; Mismatches 137; Indels 19; Gaps 9;

QY 4 PTVKILQSCDGGHPPTIQLLCLVSGYTGTTNITWLQEDQVMDVLDSTAS-TTQGE 62
DB 251 PTVEILQGPCASS-----ESVELLCLITGYAPSEIKVQWLNQGVTEISPSNKPCKEEND 306
QY 63 LASTQSELTLSQKHLSDRTYTCQVYQGHF-FEDSTKCCADS--NPRGVSAYLSPSP 118
DB 307 TFSRSKSVKVPEDWNSGDSYTKVTHPASHYKTEASTKCCDDTAITPK---VDVLPPSP 363
QY 119 FDLFIKRSPTITCLVVDLAPSKGTVNLTWRSAGKPVNHSTRKEBKORNGTLTVTSTLPV 178
DB 364 KDLVTKKAVYC-VISRMTSTDLLTVQWSRSDGKKALAFDSAPKAYDGTFTVKSTLKI 422
QY 179 GTRDWIEGTQYQVRVTHPHLPALMRSTTKTGSPRAAPEVYAFATPEWPGSRDKRTLACL 238
DB 423 SPGDWENKQFNCKVHPDLPSPIEKSIQKQSDPGTEPTITLLPPSDDDELNDIFSLICW 482
QY 239 IQNFWPDISVQWLHNEVOLPDARHSTTQPRKTGSQFFVFSRLVETRAEWEQKDEFIC 297
DB 483 LKNFRPQDLYVFWKDGVTLEEDYNTTTPVLEEEEGFISFKLTIARSDWNRGATYSC 542
QY 298 RAVHEAASPSQTVQRAVSNVPG 320
DB 543 IAAHNTIS-----QRDIKKNRGK 560

RESULT 5
Q95M34 HORSE PRELIMINARY; PRT; 337 AA.
ID Q95M34 HORSE PRELIMINARY;
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Immunoglobulin gamma 1 heavy chain constant region (fragment).
GN Name=IGHC1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199:105-118(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22172648; PubMed=12185539; DOI=10.1007/s00251-002-0458-4;
```

RA Wagner B., Greiser-Wilke I., Wege A.K., Radbruch A., Leibold W.;
RT "Evolution of the six horse IGHG genes and corresponding
RL immunoglobulin gamma heavy chains.";
DR EMBL; AJ300675; CAC44624.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; UNKOWN 2.
FT CHAIN <1 337 immunoglobulin gamma 1 heavy chain
FT NON TER 1
FT SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
SQ
Query Match 26.3%; Score 448.5; DB 2; Length 337;
Best Local Similarity 31.3%; Pred. No. 1.3e-27;
Matches 106; Conservative 62; Mismatches 146; Indels 25; Gaps 8;
QY 2 TPPTVKIIQSSCDGGHFFPTIQLCLVSGYTPGTINITWLEDGQWMDVLTSTATTQEG 61
Db 4 TAPKYFALAPGC--GTTSDSTVALGCLVSGYFPPEPVKVSWS--NSGSLTSGVHTFSPVLQSS 60
QY 62 ELASTQSELTLSQKWLSDRTYTCOVYQGHTE-----DSTKKCADSN--PR--- 107
Db 61 GFYSLSMVTVPASTWTSE--TVICNVVHAASNFKVDKRIEPIPDNHQKVCMDSCPKCPA 119
QY 108 -----GVSAIYLRSPED--LFIKSPITITCLVLDLAPSKGTVNLWTSRASGKPVNHSR 161
Db 120 PELLGGSPVFPFPKDTMLTRTPEVTCVVDVSVQENPDVKFNWMDGVEVTRATTRP 179
QY 162 BEKQNGTLTVTSLFVGTDRWIEGETYQCRVTHPLPALMRSTTKTGSPRAPEVYAF 221
Db 180 KEEQFNSTVRVSVLRIHQDWLSGKEPKCKVNNQALPQPIERTITTKGRSQEPQVYVL 239
QY 222 ATPWPGGRDKTACLQNFPEDISVQWLHNEVQLDARHSTTPQRTKSGGFVFSR 281
Db 240 APHPDELKSKSVTCLVKDFPPEINIEWQSNQGOPELETKYSTTAAQQSDGSGFYLSK 299
QY 282 LEVTRAWEOKDEFICRAVHEAASPSQTQVORASVNP 320
Db 300 LSVDRNRWQGGTFTTCGVNHEALHNYT--QKNVSKNPGK 337
RESULT 6
MUC_MOUSE STANDARD; PRT; 454 AA.
AC P01872;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig mu chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81076590; PubMed=6255422;
RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
RT comparison with other immunoglobulin heavy chain genes.";
RL Nucleic Acids Res. 8:3933-3945(1980).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82051295; PubMed=6795090; DOI=10.1016/0378-1119(81)90102-5;
RA Goldberg G.I., Vanin E.F., Zrolka A.M., Blattner F.R.;
RT "Sequence of the gene for the constant region of the mu chain of
RT Balb/c mouse immunoglobulin.";

RL Gene 15:33-42(1981).
RN [3]
RP NUCLEOTIDE SEQUENCE (MVELOMA TEPC183).
RX MEDLINE=81185562; PubMed=6260591; DOI=10.1016/0378-1119(80)90017-7;
RA Auffray C., Rougeon F.;
RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu
RT chain of mouse immunoglobulin.";
RL Gene 12:77-86(1980).
RN [4]
RP PROTEIN SEQUENCE (MVELOMA PROTEIN MOPC 104E).
RX MEDLINE=79223904; PubMed=111247;
RA Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.;
RT "Amino acid sequence of a mouse immunoglobulin mu chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
RN [5]
RP SEQUENCE REVISION (MOPC 104E).
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=During differentiation, B lymphocytes switch from
CC expression of isoform Membrane-bound to isoform Secreted;
CC Name=Secreted;
CC IsoId=P01872-1; Sequence=Displayed;
CC Name=Membrane-bound;
CC IsoId=P01873-1; Sequence=External;
CC -----
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CC -----
DR EMBL; J00443; AAB59650.1; -; Genomic DNA.
DR EMBL; J00444; AAB59650.1; JOINED; Genomic DNA.
DR EMBL; V00827; -; NOT_ANNOTATED_CDS; mRNA.
DR PIR; A02166; MHMS.
DR HSSP; P01861; 1ADQ.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR GO; GO:0019815; C:B cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0000187; P:activation of MAPK; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . . ; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00407; IGC1; 4.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 3.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
FT REGION <1 104
FT REGION 105 216
FT REGION 217 323
FT REGION 324 435
FT REGION 436 454
FT C-terminal segment of secreted form.

FT CARBOHYD 45 45 N-linked (GlcNAc...).

FT CARBOHYD 210 210 N-linked (GlcNAc...).

FT CARBOHYD 242 242 N-linked (GlcNAc...).

FT CARBOHYD 280 280 N-linked (GlcNAc...).

FT CARBOHYD 441 441 N-linked (GlcNAc...).

FT DISULFID 13 13 Interchain (with light chain) (Probable).

FT DISULFID 27 27 Interchain (with light chain) (Probable).

FT DISULFID 135 135 By similarity.

FT DISULFID 215 215 Interchain (with heavy chain) (Probable).

FT DISULFID 245 245 By similarity.

FT DISULFID 292 292 Interchain (with heavy chain) (Probable).

FT DISULFID 352 352 By similarity.

FT DISULFID 453 453 Interchain (with heavy chain) (Probable).

FT VARIANT 77 77 S -> N (in MOPC 104E).

FT VARIANT 100 100 H -> Q (in MOPC 104E).

FT VARIANT 225 225 T -> N (in TPC183 and MOPC 104E).

FT VARIANT 257 257 N -> S (in TPC183).

FT VARIANT 257 257 N -> T (in MOPC 104E).

FT VARIANT 367 367 L -> K (in TPC183 and MOPC 104E; requires 2 nucleotide substitutions).

FT NON_TER 1 1

SQ SEQUENCE 454 AA; 49972 MW; EBCCA6B8569AEB5 CRC64;

Query Match 25.7%; Score 439.5; DB 1; Length 454;

Best Local Similarity 32.3%; Pred. No. 9.8e-27;

Matches 106; Conservative 57; Mismatches 152; Indels 13; Gaps 8;

Qy 4 PTVKLOSSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTTQGE 62

Db 111 PNVNVPVPPRDFSGPAPRKSCLICEATNTPKPIVSWLKDGLVESGFTDPVTIENK 170

Qy 63 LASTQ-----SELTLSQKHLSDRTYTCQVYQGHF-EDSTKCADSNPRGVSAYLSRP 116

Db 171 GSTPQTYKVISTLTITSEIDNLNLNVYTCRVDHRGLTFLKNVSTCAASPTDILTFTIPP 230

Qy 117 SPFDLFRKSPITICLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKQKNGTLTSTL 176

Db 231 SFADIFLSKANLTCVLSNLTATYE-TLNISWASQSQGEPLTKIKIMESHNGFTSAKVA 289

Qy 177 PVGTRDWIEGTYQCRVTHPLRALMRSTTKTSGPRAAPEVYAFATP--EWPGRDKRT 234

Db 290 SVCVEDNNRKEFVCTVTRDLSPQKFKISKNEVHKHPAVYLLPPAREQLNRESAT 349

Qy 235 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKGS-GF-FVFSRLVETRAWEOK 292

Db 350 VTCLVKGFSPADISVQWLQGLLPQEKYVTSAPMPGPGAGFYFTHSILTVTEEWNSG 409

Qy 293 DEFTICRAVHAASPSQTVORAVSNPGK 320

Db 410 ETTYTCVVGHEAL-PHLVTERTVDKSTGK 436

RESULT 7

Q4V9V8_MOUSE PRELIMINARY; PRT; 590 AA.

AC Q4V9V8_MOUSE PRELIMINARY; PRT; 590 AA.

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN Name=Igh-6;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Mammary gland.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Mammary gland;

RG NIH MGC Project;

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC096667; AAH96667.1; -; mRNA.

DR MGI; MGI:96448; Igh-6.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 4.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 4.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 5.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.

KW Hypothetical protein.

SQ SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;

Query Match 25.7%; Score 439.5; DB 2; Length 590;

Best Local Similarity 32.3%; Pred. No. 1.4e-26;

Matches 106; Conservative 57; Mismatches 152; Indels 13; Gaps 8;

Qy 4 PTVKLOSSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTTQGE 62

Db 247 PNVNVPVPPRDFSGPAPRKSCLICEATNTPKPIVSWLKDGLVESGFTDPVTIENK 306

Qy 63 LASTQ-----SELTLSQKHLSDRTYTCQVYQGHF-EDSTKCADSNPRGVSAYLSRP 116

Db 307 GSTPQTYKVISTLTITSEIDNLNLNVYTCRVDHRGLTFLKNVSTCAASPTDILTFTIPP 366

Qy 117 SPFDLFRKSPITICLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKQKNGTLTSTL 176

Db 367 SFADIFLSKANLTCVLSNLTATYE-TLNISWASQSQGEPLTKIKIMESHNGFTSAKVA 425

Qy 177 PVGTRDWIEGTYQCRVTHPLRALMRSTTKTSGPRAAPEVYAFATP--EWPGRDKRT 234

Db 426 SVCVEDNNRKEFVCTVTRDLSPQKFKISKNEVHKHPAVYLLPPAREQLNRESAT 485

Qy 235 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKGS-GF-FVFSRLVETRAWEOK 292

Db 486 VTCLVKGFSPADISVQWLQGLLPQEKYVTSAPMPGPGAGFYFTHSILTVTEEWNSG 545

Qy 293 DEFTICRAVHAASPSQTVORAVSNPGK 320

Db 546 ETTYTCVVGHEAL-PHLVTERTVDKSTGK 572

RESULT 8

Q4KML5_MOUSE PRELIMINARY; PRT; 617 AA.

ID Q4KML5_MOUSE PRELIMINARY; PRT; 617 AA.

AC Q4KML5;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)


```

QY 235 LACLIQNFMPEDISVQWLHNEVOLPDARHSTTOPRTKGS-GF-FVFSRLVETRAEWEQK 292
Db 489 VTCVLVGFSPADISVQWLQKQLPQKVTSPAMPPEPGAGFYFTHSILTVTEEWNSG 548
QY 293 DEFICRAVHEAASPSQTVQRAV 314
Db 549 ETYTCVVSHEAL-PHLVTERTV 569

RESULT 10
MUCM MOUSE
ID MUCM MOUSE STANDARD; PRT; 475 AA.
AC P01873;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RX MEDLINE=81076590; PubMed=6255422;
RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
RL comparison with other immunoglobulin heavy chain genes.";
RL Nucleic Acids Res. 8:3933-3945(1980).
RN [2]
RX NUCLEOTIDE SEQUENCE OF 432-475.
RA Early P., Rogers J., Davis M., Calame K., Bond M., Wall R., Hood L.;
RT "Two mRNAs can be produced from a single immunoglobulin mu gene by
RL alternative RNA processing pathways.";
RL Cell 20:313-319(1980).
RN [3]
RX NUCLEOTIDE SEQUENCE OF 409-475 (MYELOMA MOPC 104E).
RA Rogers J., Early P., Carter C., Calame K., Bond M., Hood L., Wall R.;
RT "Two mRNAs with different 3' ends encode membrane-bound and secreted
RL forms of immunoglobulin mu chain.";
RL Cell 20:303-312(1980).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=During differentiation, B lymphocytes switch from
CC expression of isoform Membrane-bound to isoform Secreted;
CC Name=Membrane-bound;
CC IsoId=P01873-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01872-1; Sequence=External;
CC -1- MISCELLANEOUS: The sequence of residues 1-409 is assumed to be
CC identical with the corresponding region of the secreted form.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00443; AB59651.1; -; Genomic DNA.
CC EMBL; J00444; AB59651.1; JOINED; Genomic DNA.
CC EMBL; V00821; CAA24202.1; -; mRNA.
CC PIR; A02167; MHMSM.
CC HSSP; P01861; IADQ.
CC GO; GO:0019815; C: B cell receptor complex; IDA.
CC GO; GO:0009897; C: external side of plasma membrane; IDA.
CC GO; GO:0042571; C: immunoglobulin complex, circulating; IDA.
CC GO; GO:0048471; C: perinuclear region; IDA.
CC GO; GO:0003623; F: antigen binding; IDA.
CC GO; GO:0005515; F: protein binding; IPI.
CC GO; GO:0004888; F: transmembrane receptor activity; IDA.
CC GO; GO:0000187; P: activation of MAPK; IDA.

QY 293 DEFICRAVHEAASPSQTVQRAV 314
Db 410 ETYTCVVGHEAL-PHLVTERTV 430

RESULT 11
Q8VCX7_MOUSE
ID Q8VCX7_MOUSE PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;

GO; GO:0030333; P: antigen processing; IDA.
GO; GO:0059853; P: B cell receptor signaling pathway; IDA.
GO; GO:0045022; P: early endosome to late endosome transport; IDA.
GO; GO:0016064; P: humoral defense mechanism (sensu Vertebrata); IDA.
GO; GO:0030890; P: positive regulation of B cell proliferation; IDA.
GO; GO:0045807; P: positive regulation of endocytosis; IDA.
GO; GO:0050731; P: positive regulation of peptidyl-tyrosine ph. . .; IDA.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG-cl.
InterPro; IPR003006; IG_MHC.
Pfam; PF07654; C1-set; 4.
SMART; SM00407; IGC1; 4.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
KW Alternative splicing; Glycoprotein; Immunoglobulin C region;
KW Immunoglobulin domain; Transmembrane.
FT TRANSMEM 455 472 Potential.
FT REGION <1 104 CH1.
FT REGION 105 216 CH2.
FT REGION 217 323 CH3.
FT REGION 324 435 CH4.
FT CARBOHYD 45 45 N-linked (GlcNAc. . .).
FT CARBOHYD 210 210 N-linked (GlcNAc. . .).
FT CARBOHYD 242 242 N-linked (GlcNAc. . .).
FT CARBOHYD 280 280 N-linked (GlcNAc. . .).
FT DISULFID 13 13 Interchain (with light chain) (Probable).
FT DISULFID 27 88 By similarity.
FT DISULFID 135 198 Interchain (with heavy chain) (Probable).
FT DISULFID 215 215 By similarity.
FT DISULFID 245 304 Interchain (with heavy chain) (Probable).
FT DISULFID 292 292 By similarity.
FT DISULFID 352 414
FT NON_TER 1
SQ SEQUENCE 475 AA; 52527 MW; F2163AD4517E1485 CRC64;

Query Match 25.2%; Score 430.5; DB 1; Length 475;
Best Local Similarity 32.3%; Pred. No. 5.5e-26;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTVKIQSCDG-GGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVLDLSTASTTQGE 62
Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSLWKDGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWSLDRVTYTCOVTVQGHTE-EDSTKKCADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNLVNVTCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLFIKSPITICLVVDLAPSKGTNLTWSRASKPVNHSRKEEKQKNGTLTVTSTL 176
Db 231 SPADIFLSKANLTCVLSNLTATYE-TLNSISWASQSGEPLTKIKIMESHNGTFSKAGVA 289
QY 177 PVGTRDWIEGTYQCRVTHPHLPRLMRSTTTKTSGRAPAEVYAFATP--EHWGSDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTQPKTKGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVKGFSPADISVQWLQKQLPQKVTSPAMPPEPGAGFYFTHSILTVTEEWNSG 409

QY 293 DEFICRAVHEAASPSQTVQRAV 314
Db 410 ETYTCVVGHEAL-PHLVTERTV 430

Query Match 25.2%; Score 430.5; DB 1; Length 475;
Best Local Similarity 32.3%; Pred. No. 5.5e-26;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

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OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.A., Rodrigues S., Sanchez A.,
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2464031;
 RA Sikder S.K., Borden P., Gruzo F., Akolkar P.N., Bhattacharya S.B.,
 RA Morrison S.L., Kabat E.A.;
 RA "Amino acid substitutions in VH CDR2 change the idiotype but not the
 antigen-binding of monoclonal antibodies to alpha(1----6)dextran.";
 RL J. Immunol. 142:888-893(1989).
 DR EMBL; BC018315; AAH18315.1; -; mRNA.
 DR PIR; C30562; C30562.
 DR HSSP; P01751; IAGW.
 DR Ensembl; ENSMUSG00000054328; Mus musculus.
 DR MGI; MGI:96448; Igh-6.
 DR GO; GO:0019815; C:B cell receptor complex; IDA.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
 DR GO; GO:0048471; C:perinuclear region; IDA.
 DR GO; GO:0003823; F:antigen binding; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
 DR GO; GO:0000187; P:activation of MAPK activity; IDA.
 DR GO; GO:0030333; P:antigen processing; IDA.
 DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.
 DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
 DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
 DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.
 DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
 DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . .; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 613 AA, 67855 MW, 41A9384DDA422862 CRC64;

Query Match 25.2%; Score 430.5; DB 2; Length 613;
 Best Local Similarity 32.3%; Pred. No. 7.6e-26;
 Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;
 QY 4 PTVKILQSSCDG-GGHFPPTIQLCLVSGVTPGTINITWLEDGQVMDVLDLSTASTTQEGE 62
 DB 249 PNVNVFVPRDGFSGPAPRKSCLICEATNFTPKPTVSWLKGKLVESGFTTDPVTIENK 308
 QY 63 LASTQ-----SELTLSQKHWSLDRYTCQVYQCHTF-EDSTKKCADSNPRGVSAIYLSRP 116
 DB 309 GSTPTQYKVVSTITISIDWNLNVYTCRVDRHGLTFLKNVSSCAASPSDILTFTIPP 368
 QY 117 SPFDLFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKEKQKNGTUTVTSTL 176
 DB 369 SFADIFLKSANLTCLVSNLATVE-TLNIWSQSGSPLETKIKIMESHNPNGTFSAKGVA 427
 QY 177 PVGTRDWIEGTQCRVTHPHLPALMRSTTKTSGPRAAEVYAFATP--EMPGRDKRT 234
 DB 428 SVCVEDWNNRKEFVCTVTHRDLPSQPKFKISKPNVHKHPAVYLLPPAREQLNRESAT 487
 QY 235 LACLQNFMPEDISVQWLHNEVQLPDRHSTTOPRTKGS-GF-FVFSRLVETVRAEWEQK 292
 DB 488 VTCLVKGFSADISVQWLQGLLPQEKYVTSAPMPEFGAPGFYFTHSILTVTEENSG 547
 QY 293 DEFICRAVHEAASPSQTVQRAV 314
 DB 548 EYTCVVGHEAL-PHLVTERTV 568
 RESULT 12
 ID Q504M7 MOUSE PRELIMINARY; PRT; 616 AA.
 AC Q504M7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.A., Rodrigues S., Sanchez A.,
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC094936; AAH94936.1; -; mRNA.
 DR InterPro; IPR003599; Ig.


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FT REGION 106 218 CH2.
FT REGION 219 324 CH3.
FT REGION 325 454 CH4.
FT CARBOHYD 45 45 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 112 112 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 192 192 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 238 238 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 257 257 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 280 280 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 441 441 N-linked (GlcNAc...) (Potential).
FT DISULFID 13 13 Interchain (with light chain) (Probable).
FT DISULFID 27 88 By similarity.
FT DISULFID 135 198 By similarity.
FT DISULFID 215 215 Interchain (with heavy chain) (Probable).
FT DISULFID 245 304 By similarity.
FT DISULFID 292 292 Interchain (with heavy chain) (Probable).
FT DISULFID 352 414 By similarity.
FT DISULFID 453 453 Interchain (with heavy chain) (Probable).
FT NON_TER 1 1
SQ SEQUENCE 454 AA; 50197 MW; 4D2134612BE1469 CRC64;

Query Match 24.8%; Score 423.5; DB 1; Length 454;
Best Local Similarity 31.5%; Pred. No. 1.9e-25;
Matches 106; Conservative 56; Mismatches 145; Indels 29; Gaps 10;

QY 4 PTVKILQSSDGG-GGHFPPTQLCLVSGYTPGTINITWLEDGQVMDVLSTASTQGE 62
DB 111 PNVSVFVPSDAFSGAPAPKSRFLCEASNFSPKQITVSWLRDGRPKVSGFTFETPEDR 170
QY 63 LASTQ-----SELTLSQKHLSDRYTCQVYQGHTR-EDSTKKCADSNRGSAYLSRP 116
DB 171 GSGRTYKIVSTLTITSEDLNLSVYTCVRDHRGLTFWKNSSVSCAASPSTIDIAFP 230
QY 117 SPFDLFIKSPITITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEQRNGTLTFTSTL 176
DB 231 SFVGIKFLNKSATLTCLVNLA-TYDTLNISSRSRSGEPLTKTLTESHNGTFSAGEA 289
QY 177 PVGTRDWIEGETYQCRVTHPLPALMRSTTKTSQPR-----AAPVYAFATPEWPGSRDK 232
DB 290 NVCVEDMDSGKEFVCTVTHRLPSQPKFISK---PREMNKTPPAVY-----QQPLAREQ 341
QY 233 -----RTLACLIONFPEDISVQWLHNEVOLPDARHSTTOPRKTGSG--FFVFSRLEV 284
DB 342 LILRESATVTCVLVKGFSADIPVQMLQKQPSQDKYVTSAPMPQPAPHLYFTHSVLT 401
QY 285 TRAEWEQKDEFTICRAVHEAASPSQTVQRAVSVNPGK 320
DB 402 TEEWNSGETYTCVVGHEAL-PHMVTERTVDRSTCK 436

RESULT 15
Q6P6C4 HUMAN
ID Q6P6C4_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6P6C4; 20-465.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDDB9348ADC37E6D CRC64;

Query Match 24.7%; Score 421; DB 2; Length 465;
Best Local Similarity 31.1%; Pred. No. 3.1e-25;
Matches 106; Conservative 61; Mismatches 138; Indels 36; Gaps 11;

QY 6 VKILQSSCDGGGHP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLSTA 55
DB 135 VTVSSASTKGSVPFLAPCSRSTSESTAALCLVKDYFPEPTVSW-NSGALTSGVHTFP 193
QY 56 STTGEGELASTQSELTLSQKHLSDRYTCQVYQ-GHTFEDST---KKCADSNP----- 106
DB 194 AVLQSSGLYSLSVYTPVPSNF-GTQYTCNVDRHKPSNTKYDKTVERKCCVECPCPAPP 252
QY 107 -RGVSAYLSRSPFD-LPIRKSPITITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEK 164
DB 253 VAGSVFLFPKPKDNTLMISRTPEVTCVVDVSHEDDEVQFNWYVDGVEVHNKTPREE 312
QY 165 QRNGTLTVTSTPLVGRDWIEGETYQCRVTHPLPALMRSTTKTSQPRAAPEVYAFATP 224
DB 313 QFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL--- 369
QY 225 EWPGRDKRT-----LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVF 279
DB 370 --PPSRBEEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYNTTTPMILDSGSGFFLY 425
QY 280 SRLVETRAEWQKDEFTICRAVHEAASPSQTVQRAVSVNPGK 320
DB 426 SKLTVDKSRWQQGNVFCSCVMHEALHNYT-QKSLSLSPGK 465

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Job time : 178.232 secs
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:51:35 : Search time 38.2609 Seconds
(without alignments)
691.469 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	331	2	US-09-401-636-1
2	1701	99.6	325	2	US-09-701-623C-1
3	1158	67.8	222	2	US-10-211-948-2
4	1146	67.1	222	2	US-10-211-948-8
5	1038.5	60.8	342	2	US-09-401-636-8
6	956.5	56.0	426	1	US-08-336-583-2
7	956.5	56.0	426	4	PCT-US95-13795-2
8	949.5	55.6	431	2	US-09-479-614-14
9	949.5	55.6	496	2	US-09-479-614-2
10	949.5	55.6	496	2	US-09-479-614-29
11	895.5	52.5	312	2	US-09-701-623C-2
12	827	48.4	341	2	US-09-401-636-11
13	793	46.5	340	2	US-09-401-636-2
14	783	45.9	313	2	US-09-701-623C-3
15	781	45.8	341	2	US-09-401-636-3
16	770	45.1	345	2	US-09-401-636-10
17	751	44.0	341	2	US-09-401-636-9
18	745	43.6	341	2	US-09-401-636-4
19	744	43.6	504	2	US-09-091-645C-2
20	744	43.6	676	2	US-09-091-645C-4
21	720	42.2	341	2	US-09-401-636-6
22	716.5	42.0	342	2	US-09-401-636-5
23	709.5	41.6	343	2	US-09-401-636-7
24	691.5	40.5	313	2	US-09-701-623C-4
25	678.5	39.7	561	2	US-09-192-545-2
26	597	35.0	113	1	US-08-232-539D-56
27	587	34.4	110	1	US-08-399-108A-6

28	587	34.4	110	1	US-08-433-105A-6	Sequence 6, Appli
29	587	34.4	110	1	US-08-434-869A-6	Sequence 6, Appli
30	581	34.0	109	1	US-08-037-579A-2	Sequence 2, Appli
31	581	34.0	109	2	US-08-601-184-2	Sequence 2, Appli
32	566.5	33.2	109	2	US-08-466-163B-1	Sequence 1, Appli
33	566.5	33.2	109	2	US-09-802-096-1	Sequence 1, Appli
34	566.5	33.2	109	2	US-09-802-077-1	Sequence 1, Appli
35	566.5	33.2	109	2	US-09-925-179-1	Sequence 1, Appli
36	556	32.6	106	1	US-08-232-539D-54	Sequence 54, Appli
37	526	30.8	119	1	US-08-464-025A-1	Sequence 1, Appli
38	508.5	29.8	118	2	US-08-466-151-1	Sequence 1, Appli
39	481.5	28.2	334	1	US-08-646-981-16	Sequence 17, Appli
40	480.5	28.1	474	2	US-09-828-995B-17	Sequence 16, Appli
41	477.5	28.0	352	2	US-09-828-995B-38	Sequence 38, Appli
42	476.5	27.9	375	2	US-09-828-995B-32	Sequence 32, Appli
43	476.5	27.9	473	2	US-09-828-995B-20	Sequence 20, Appli
44	472.5	27.7	470	2	US-09-828-995B-11	Sequence 11, Appli
45	468.5	27.4	468	2	US-09-828-995B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1

Query Match		100.0%	Score 1707;	DB 2;	Length 331;
Best Local Similarity		100.0%	Pred. No. 3.3e-156;	Mismatches 0;	Indels 0; Gaps 0;
Matches 320;		Conservative			
Qy	1	FTPTVKILOSCDGGGHPPTIOLLCIVSGVTGCTINITWLEDGQVMDVLDLSTASTTQE	60		
Db	12	FTPTVKILOSCDGGGHPPTIOLLCIVSGVTGCTINITWLEDGQVMDVLDLSTASTTQE	71		
Qy	61	GELASTQSELTLSQKHWLSDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRSPSPD	120		
Db	72	GELASTQSELTLSQKHWLSDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRSPSPD	131		
Qy	121	LFIRKSPITCLIVDLAPSKGTVALTWRSAGKPVNHSTRKEEKORNGTLTSTLPVGT	180		
Db	132	LFIRKSPITCLIVDLAPSKGTVALTWRSAGKPVNHSTRKEEKORNGTLTSTLPVGT	191		
Qy	181	RDWTEGYQCRVTHPLPRALMRSTTSGPRAPEVYAFATPEWPGSRDKRTLACLIQ	240		
Db	192	RDWTEGYQCRVTHPLPRALMRSTTSGPRAPEVYAFATPEWPGSRDKRTLACLIQ	251		
Qy	241	NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLVETRAEWEQKDEFTICRAV	300		
Db	252	NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLVETRAEWEQKDEFTICRAV	311		
Qy	301	HEAASPSQTVQRAVSVNPGK	320		
Db	312	HEAASPSQTVQRAVSVNPGK	331		

RESULT 2
US-09-701-623C-1
; Sequence 1, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
; FILE REFERENCE: 11514153U1
; CURRENT APPLICATION NUMBER: US/09/701.623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 325
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: CH2CH3 of human IgE
; PUBLICATION INFORMATION:
; AUTHORS: Dorrington,
; JOURNAL: Immunology
; VOLUME: 41
; PAGES: 3-25
; DATE: 1978
US-09-701-623C-1
Query Match 99.6%; Score 1701; DB 2; Length 325;
Best Local Similarity 99.4%; Pred. No. 1.2e-155;
Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTPTVKILSSCDGGHFPPTQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOE 60
Db 6 FTPTVKILSSCDGGHFPPTQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOE 65
Qy 61 GELASTOSELTLSQKWLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPFD 120
Db 66 GELASTOSELTLSQKWLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPFD 125
Qy 121 LFIKSPITITCLVVDLAPSKGTVNLWTSRASKGPKVNHSTRKEKQRNGTLTVTSTLPVGT 180
Db 126 LFIKSPITITCLVVDLAPSKGTVNLWTSRASKGPKVNHSTRKEKQRNGTLTVTSTLPVGT 185
Qy 181 RDWIEGTQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 186 RDWIEGTQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245
Qy 241 NMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRLVTRAEWEQKDEFICRAV 300
Db 246 NMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRLVTRAEWEQKDEFICRAV 305
Qy 301 HEAASPSTQVQRAVSNVPGK 320
Db 306 HEAASPSTQVQRAVSNVPGK 325
RESULT 3
US-10-211-948-2
; Sequence 2, Application US/10211948
; Patent No. 6889145
; GENERAL INFORMATION:
; APPLICANT: Jardtetzky, Theodore S.
; APPLICANT: Wurzburg, Beth A.
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A FC REGION OF AN IGE ANTIBODY AND USE THEREOF
; FILE REFERENCE: AL-9-C3
; CURRENT APPLICATION NUMBER: US/10/211,948

; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 09/809,746
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-948-2
Query Match 67.8%; Score 1158; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.6e-103; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 103 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASKGPKVNHSTRKE 162
Db 5 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASKGPKVNHSTRKE 64
Qy 163 EKQRNGTLTVTSTLPVGTDRDWEIETGYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF 222
Db 65 EKQRNGTLTVTSTLPVGTDRDWEIETGYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF 124
Qy 223 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 282
Db 125 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 184
Qy 283 EVTRAWEQKDEFICRAVHEAASPSTQVQRAVSNVPGK 320
Db 185 EVTRAWEQKDEFICRAVHEAASPSTQVQRAVSNVPGK 222
RESULT 4
US-10-211-948-8
; Sequence 8, Application US/10211948
; Patent No. 6889145
; GENERAL INFORMATION:
; APPLICANT: Jardtetzky, Theodore S.
; APPLICANT: Wurzburg, Beth A.
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A FC REGION OF AN IGE ANTIBODY AND USE THEREOF
; FILE REFERENCE: AL-9-C3
; CURRENT APPLICATION NUMBER: US/10/211,948
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 09/809,746
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-948-8
Query Match 67.1%; Score 1146; DB 2; Length 222;
Best Local Similarity 99.1%; Pred. No. 2.3e-102; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 103 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASKGPKVNHSTRKE 162
Db 5 DSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASKGPKVNHSTRKE 64
Qy 163 EKQRNGTLTVTSTLPVGTDRDWEIETGYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF 222
Db 65 EKQRNGTLTVTSTLPVGTDRDWEIETGYQCRVTHPLPALMRSTTKTSGPRAAPEVYAF 124
Qy 223 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 282
Db 125 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 184
Qy 283 EVTRAWEQKDEFICRAVHEAASPSTQVQRAVSNVPGK 320
Db 185 EVTRAWEQKDEFICRAVHEAASPSTQVQRAVSNVPGK 222

RESULT 5
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match 60.8%; Score 1038.5; DB 2; Length 342;
Best Local Similarity 62.4%; Pred. No. 9.9e-92;
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 3 PPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQ 60
DB 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVWLVLDGQEAENLFPVTPRKREG 81

QY 61 GELASTQSELTLSQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSRPSPPD 120
DB 82 GQTFSLQSEVNIQGMWSSNTYTCVYQGHFTFEDSTKCADSNPRGVSAYLSRPSPPD 141

QY 121 LFIKSPITICLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTWTSLPVG 180
DB 142 LFIKSPITICLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTWTSLPVG 201

QY 181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACL 239
DB 202 RDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPDEETGT--TRIVTCL 259

QY 240 QNFMPEDISVQWLHNEVQLPDARHSTTPQRTKGS--GFFVFSRLEVTRAWEQKDFIC 297
DB 260 RGFYFSEISVQWLHNEEDHTGHTTTRPQKHGTDPSFFLYSRMLVNKSIWEKGNLVC 319

QY 298 RAVHEAASPSQTVQRAVSNPG 319
DB 320 RVVHEALPGSRTLEKSLHYSAG 341

RESULT 6
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PC-DOS/MS-DOS
; FILING DATE:

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-583-2

Query Match 56.0%; Score 956.5; DB 1; Length 426;
Best Local Similarity 56.2%; Pred. No. 1.1e-83;
Matches 182; Conservative 50; Mismatches 87; Indels 5; Gaps 4;

QY 1 FTPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59
DB 104 FIPPTVKLFHSSCNFPGDHTTITQLCLISGYVPGDMEVWLVDGQKATNIFPYTAPCTK 163

QY 60 EGELASTQSELTLSQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSRPSPF 119
DB 164 EGNVTSTHSELNIQGEWVSQKTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSRPSPL 223

QY 120 DLFIKSPITICLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTWTSLPVG 179
DB 224 DLYVHKAPKTCVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTWTSLPVG 282

QY 180 TRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-ENPGSRDKRTLACL 238
DB 283 TNDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPDEETGT--TRIVTCL 342

QY 239 IQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKGS--GFFVFSRLEVTRAWEQKDFI 296
DB 343 IQNFMPEDISVQWLHNEEDHTGHTTTRPQKHGTDPSFFLYSRMLVNKSIWEKGNLVC 402

QY 297 RAVHEAASPSQTVQRAVSNPGK 320
DB 403 QVVVHEALSGSRILQKRWVSKTPGK 426

RESULT 7
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:

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;
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 56.08; Score 956.5; DB 4; Length 426;
Best Local Similarity 56.2%; Pred. No. 1.1e-83;
Matches 182; Conservative 50; Mismatches 87; Indels 5; Gaps 4;

QY 1 FTPPTVKILQSSCDGGHFPPTIQLLCLISGVYPGDMEVTLVLDGQKATNIFYPTAPGK 59
DB 104 FIPTVKLFHSSCNPNVGDTHITIIQLLCLISGVYPGDMEVTLVLDGQKATNIFYPTAPGK 163
QY 60 EGE LASTQS E L T S Q K H W L S D R Y T T C Q V T Y O G H T F E D S T K K C A D S N P R G V S A Y L S R P S P F 119
DB 164 E G N V T S H S E L N I T Q G E W S Q K Y T T C Q V T Y O G H T F E D S T K K C A D S N P R G V S A Y L S R P S P L 223
QY 120 D L F I R K S P T I T C L V D L A P S K G T V N L T W S R A S G K P V N H S T R K E E K Q R N G T L T V T S T L P V G 179
DB 224 D L Y V H K A P K I T C L V D L A P S K G T V N L T W S R A S G K P V N H S T R K E E K Q R N G T L T V T S T L P V N 282
QY 180 T R D W I E G E T Y Q C R V T H P H L P R A L M R S T T K T S G P R A A P E V Y A F A T P - E W P G S R D K R T L A C L 238
DB 283 T N D W I E G E T Y C R V T H P H L P K D I V R S I A K A P G R A P D V Y L F L P P E E Q G T K D R V I L T C L 342
QY 239 I Q N F M P E D I S V Q W L H N E V Q L P D A R H S T T Q P R K T G S - - S G F F V F S R L E V T R A E W E Q K D E F I 296
DB 343 I Q N F F P A D I S V Q W L R N D S P I Q D Y T T T G P H K V S G S R P A F F I F S R L E V S R V D W E Q K N K F T 402
QY 297 C R A V H E A A S P S Q T V O R A V S V N P G K 320
DB 403 C Q V V H E A L S G S R I L Q K W S K T P G K 426

RESULT 8
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 55.6%; Score 949.5; DB 2; Length 431;
Best Local Similarity 56.5%; Pred. No. 5.3e-83;
Matches 183; Conservative 46; Mismatches 90; Indels 5; Gaps 4;

QY 1 FTPPTVKILQSSCDGGHFPPTIQLLCLISGVYPTGTTNITWLEDGQ-VMDVDLSTASTTQ 59
DB 174 FIPTVKLFHSSCNPLGDTGSHIQLLCLISGVYPGDMEVTLVLDGQKATNIFYPTAPGKQ 233
QY 60 EGE LASTQS E L T S Q K H W L S D R Y T T C Q V T Y O G H T F E D S T K K C A D S N P R G V S A Y L S R P S P F 119
DB 234 E G K V T S H S E L N I T Q G E W S Q K Y T T C Q V T Y O G H T F E D H A R K C T E S D P R G V S Y L S P S P L 293
QY 120 D L F I R K S P T I T C L V D L A P S K G T V N L T W S R A S G K P V N H S T R K E E K Q R N G T L T V T S T L P V G 179
DB 294 D L Y V H K S P K I T C L V D L A N T D G M I - L T W S R E N G E S V H P D P M V K T Q Y N G T I T V T S T L P V D 352
QY 180 T R D W I E G E T Y Q C R V T H P H L P R A L M R S T T K T S G P R A A P E V Y A F A T P E W - P G S R D K R T L A C L 238
DB 353 A T D W E G E T Y Q C K V T H P D L P K D I V R S I A K A P G R R P P P E V I V L P P E G E P K T K D K V I L T C L 412
QY 239 I Q N F M P E D I S V Q W L H N E V Q L P D A R H S T T Q P R K T G - - S G F F V F S R L E V T R A E W E Q K D E F I 296
DB 413 I Q N F F P P D I S V Q W L H N D S P V R T E Q A T T W P H K A T G S P A F F V F S R L E V S R A D W E Q R D V F T 472
QY 297 C R A V H E A A S P S Q T V O R A V S V N P G K 320
DB 473 C Q V V H E A L P G F R T L K K S V S K N P G K 496
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DB 109 FIPTVKLFHSSCNPLGDTGSHIQLLCLISGVYPGDMEVTLVLDGQKATNIFYPTAPGKQ 168
QY 60 EGE LASTQS E L T S Q K H W L S D R Y T T C Q V T Y O G H T F E D S T K K C A D S N P R G V S A Y L S R P S P F 119
DB 169 E G K V T S H S E L N I T Q G E W S Q K Y T T C Q V T Y O G H T F E D H A R K C T E S D P R G V S Y L S P S P L 228
QY 120 D L F I R K S P T I T C L V D L A P S K G T V N L T W S R A S G K P V N H S T R K E E K Q R N G T L T V T S T L P V G 179
DB 229 D L Y V H K S P K I T C L V D L A N T D G M I - L T W S R E N G E S V H P D P M V K T Q Y N G T I T V T S T L P V D 287
QY 180 T R D W I E G E T Y Q C R V T H P H L P R A L M R S T T K T S G P R A A P E V Y A F A T P E W - P G S R D K R T L A C L 238
DB 288 A T D W E G E T Y Q C K V T H P D L P K D I V R S I A K A P G R R P P P E V I V L P P E G E P K T K D K V I L T C L 347
QY 239 I Q N F M P E D I S V Q W L H N E V Q L P D A R H S T T Q P R K T G - - S G F F V F S R L E V T R A E W E Q K D E F I 296
DB 348 I Q N F F P P D I S V Q W L H N D S P V R T E Q A T T W P H K A T G S P A F F V F S R L E V S R A D W E Q R D V F T 407
QY 297 C R A V H E A A S P S Q T V O R A V S V N P G K 320
DB 408 C Q V V H E A L P G F R T L K K S V S K N P G K 431

RESULT 9
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 55.6%; Score 949.5; DB 2; Length 496;
Best Local Similarity 56.5%; Pred. No. 6.5e-83;
Matches 183; Conservative 46; Mismatches 90; Indels 5; Gaps 4;

QY 1 FTPPTVKILQSSCDGGHFPPTIQLLCLISGVYPTGTTNITWLEDGQ-VMDVDLSTASTTQ 59
DB 174 FIPTVKLFHSSCNPLGDTGSHIQLLCLISGVYPGDMEVTLVLDGQKATNIFYPTAPGKQ 233
QY 60 EGE LASTQS E L T S Q K H W L S D R Y T T C Q V T Y O G H T F E D S T K K C A D S N P R G V S A Y L S R P S P F 119
DB 234 E G K V T S H S E L N I T Q G E W S Q K Y T T C Q V T Y O G H T F E D H A R K C T E S D P R G V S Y L S P S P L 293
QY 120 D L F I R K S P T I T C L V D L A P S K G T V N L T W S R A S G K P V N H S T R K E E K Q R N G T L T V T S T L P V G 179
DB 294 D L Y V H K S P K I T C L V D L A N T D G M I - L T W S R E N G E S V H P D P M V K T Q Y N G T I T V T S T L P V D 352
QY 180 T R D W I E G E T Y Q C R V T H P H L P R A L M R S T T K T S G P R A A P E V Y A F A T P E W - P G S R D K R T L A C L 238
DB 353 A T D W E G E T Y Q C K V T H P D L P K D I V R S I A K A P G R R P P P E V I V L P P E G E P K T K D K V I L T C L 412
QY 239 I Q N F M P E D I S V Q W L H N E V Q L P D A R H S T T Q P R K T G - - S G F F V F S R L E V T R A E W E Q K D E F I 296
DB 413 I Q N F F P P D I S V Q W L H N D S P V R T E Q A T T W P H K A T G S P A F F V F S R L E V S R A D W E Q R D V F T 472
QY 297 C R A V H E A A S P S Q T V O R A V S V N P G K 320
DB 473 C Q V V H E A L P G F R T L K K S V S K N P G K 496
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RESULT 10
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Fells catus
US-09-479-614-29

Query Match 55.6%; Score 949.5; DB 2; Length 496;
Best Local Similarity 56.5%; Pred. No. 6.5e-83;
Matches 183; Conservative 46; Mismatches 90; Indels 5; Gaps 4;

Qy 1 FPPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59
Db 174 FIPPTVKLFHSSCNPLDGTGTIQLCLISGVPGDMEVTLVDGQKATNIPPTAPGKQ 233
Qy 60 EGELASTQSELTLSQKHLSDRYTCQVYTOGHTEFEDSTKCKADSNPRGVSAYLSRSPF 119
Db 234 EKVTSHTSELNITQGEVWSQKTYTCQVYTOGHTEFEDHARKCTSDPRGVSTYLSPPSPL 293
Qy 120 DLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEKQKRGNTLTVTSTLPVG 179
Db 294 DLVYHKSPTITCLVVDLANTDGM-LTWSRENGESVHPDPMVKTKYNGTITVTSTLPVD 352
Qy 180 TRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEW-PGSRDKRTLA 238
Db 353 ATDWIEGETYQCKVTHPLPKDIVRSIAKAPGRFPPEVYVFLPPEGEPKTKDKVILTCL 412
Qy 239 IQNMPEDISVQWLHNEVQLPDARHSTTQPRKTKG--SGFFVFSRLEVTAEWEQKDFI 296
Db 413 IQNFPFDDISVQWLHNDSPVTEQQAATWPHKATGSPAFFVFSRLEVRADWEQORDVFT 472
Qy 297 CRAVHEAASPSQTVQRAVSNPGK 320
Db 473 CQVHEALPGFRTLKKSYSKNPGK 496

RESULT 11
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE

; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2

Query Match 52.5%; Score 895.5; DB 2; Length 312;
Best Local Similarity 55.1%; Pred. No. 5.3e-78;
Matches 172; Conservative 48; Mismatches 83; Indels 9; Gaps 5;

Qy 1 FPPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59
Db 6 FIPPTVKLFHSSCNPLDGTHTTQLCLISGVPGDMEVTLVDGQKATNIPPTAPGK 65
Qy 60 EGELASTQSELTLSQKHLSDRYTCQVYTOGHTEFEDSTKCKADSNPRGVSAYLSRSPF 119
Db 66 EGNVTSHTSELNITQGEVWSQKTYTC---QGFTFKDEARKCESDPRGVSTYLSPPSPL 121
Qy 120 DLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEKQKRGNTLTVTSTLPVG 179
Db 122 DLVYHKA PKITCLVVDLATMEG-MNLTYRESKEPVNPGPLNKKDHFNGLTITVTSTLPVN 180
Qy 180 TRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATP-EMPGRDKRTLA 238
Db 181 TNDWIEGETYQCRVTHPHLPKDIVRSIAKAPGRAPDPVYLFLLPPEBEQGTKDRVTLTCL 240
Qy 239 IQNMPEDISVQWLHNEVQLPDARHSTTQPRKTKG--GRFVFSRLEVTAEWEQKDFI 296
Db 241 IQNFPFADISVQWLHNDSPITQDQYTTGPHKVSGRPAFFIFSRLEVRVDMWEQKNKFT 300
Qy 297 CRAVHEAASPSQ 308
Db 301 CQVHEALSGSR 312

RESULT 12
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-11

Query Match 48.4%; Score 827; DB 2; Length 341;
Best Local Similarity 49.7%; Pred. No. 2.4e-71;
Matches 160; Conservative 58; Mismatches 96; Indels 8; Gaps 5;

Qy 3 PPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQ 60
Db 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVTVLVDGQAEMLFPYTPPKREG 81
Qy 61 EGELASTQSELTLSQKHLSDRYTCQVYTOGHTEFEDSTKCKADSNPRGVSAYLSRSPF 120
Db 82 GQTFSLQSEVNITQGMSSNTYTCVHKNGSIFEDSSRKCESDPRGVSTYLSPPSPL 141
Qy 121 LFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEKQKRGNTLTVTSTLPVGT 180
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142	LYTHKAPKTC	LVDLATWEG	-MNU	TWYRESKEPV	NGPGLNK	KDHFNGT	ITVTST	PLPVNT	200
181	RDWIEGETY	QCVRTHPHL	PRALMRST	TKTSPRAA	PEVYAF	-ATPEWPS	GRDRT	TLACLI	239
201	NDWIEGETY	CVRTHPHL	PKOIVRSI	AKLPKRLA	PEVYML	PPSP	ETGT--	TRTVC	258
240	QNFMPED	ISVQWLHNE	VQLPDARH	STQPRK	TGKS--	GFFVFR	SRLEV	TRAEWQKDE	297
259	RCGFPEI	SVQWLFNNE	DHGTGHTT	ITRPQKH	DGTDPS	FFLYSR	MLVNKS	IWEKGNLVC	318
298	RAVHEA	APSQT	VRASV	NPNG	319				
319	RVVHEAL	PGSR	TLKLS	HYSA	340				

RESULT 13

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US-09-401-636-2
; Sequence 2, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated
US-09-401-636-2

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Query Match	46.5%	Score 793;	DB 2;	Length 340;
Best Local Similarity	47.4%	Pred. No. 4.6e-68;		
Matches 152;	Conservative 54;	Mismatches 109;	Indels 6;	Gaps 5;

Qy	2	TPPVKTLQSSCDGGHFPPTIOLLCVSVGYPGTGINTWL-EDGVMDVDLSTASTQIE	60
Db	12	TKPTVDLHSSCDPNA-FHSTIQYCVYGHQNDVSIHMLMDRKIYETHAQNVLKEE	70
Qy	61	GELASTQSELTLSOKHWSLDRYTCVYTOGHTPEDTKKCADSNPRGVSAIYLSRSPFD	120
Db	71	GKLASTYSRLNIIOQWMSSESTFCKVTSOGENYWAHTRCSDDEPRGVITLIPPSPLD	130
Qy	121	LFTRKSTPTICLVVDLAPSKGTVNLTVWSRAGKPVNHSTRKEEKQRNGTLTVTSTLPGVT	180
Db	131	LYENGTEPKLTCLVLDL-ESBENITVTVWRERKKSIGSQRSTKHHNATTSITSLPVD	189
Qy	181	RDMEGETYQCRVTHPHLPALAMESTTKTSQPRAAPEVAFATPEWPGSRDKRTLACLIQ	240
Db	190	KDMIEGEGYQCRVDHPHPKPIVRSITKAPGKSAPEVYVFLPPE-BEEKDKRTLTLCLIQ	248
Qy	241	NFMPEDISVOWLHNEVOLPDAHSTTTPRKTKGSG--FFVFSRLVETRAEWEQKDEFICR	298
Db	249	NFPEDISVQWLQDSKLIPKSOHSTTTPLKNGSNQRPFFISRLVETKALMTQTKQFTCR	308
Qy	299	AVTHEAASPQTQRAVSNPG	319
Db	309	VIHEALREPKLERTISKSLG	329

RESULT 14

RESOLVED 14
US-09-701-623C-3
; Sequence 3, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph. D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION

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1  TITLE OF INVENTION:  ALLERGY
2
3  FILE REFERENCE:  11514153US1
4
5  CURRENT APPLICATION NUMBER:  US/09/701,623C
6
7  CURRENT FILING DATE:  2000-12-01
8
9  PRIOR APPLICATION NUMBER:  PCT/US99/13959
10
11 PRIOR FILING DATE:  1999-06-21
12
13 PRIOR APPLICATION NUMBER:  09/100,287
14
15 PRIOR FILING DATE:  1998-06-20
16
17 NUMBER OF SEQ ID NOS:  91
18
19 SOFTWARE:  PatentIn Ver. 2.1
20
21 SEQ ID NO 3
22
23 LENGTH:  313
24
25 TYPE:  PRT
26
27 ORGANISM:  RAT
28
29 FEATURE:
30
31 OTHER INFORMATION:  CH2CH3 of rat IgE
32
33 PUBLICATION INFORMATION:
34
35 AUTHORS:  Dorrington,
36
37 AUTHORS:  Bennich,
38
39 JOURNAL:  Immunology
40
41 VOLUME:  41
42
43 PAGES:  3-25
44
45 DATE:  1978
46
47 PUBLICATION INFORMATION:
48
49 AUTHORS:  Patel,
50
51 JOURNAL:  Immunogenetics
52
53 VOLUME:  41
54
55 PAGES:  282-286
56
57 DATE:  1995
58
59 PUBLICATION INFORMATION:
60
61 AUTHORS:  Steen,
62
63 JOURNAL:  J. Mol. Biol.
64
65 VOLUME:  177
66
67 PAGES:  19-32
68
69 DATE:  1984
70
71 PUBLICATION INFORMATION:
72
73 AUTHORS:  Ishida,
74
75 JOURNAL:  EMBO J.
76
77 VOLUME:  1
78
79 PAGES:  1117-1123
80
81 DATE:  1982
82
83 US-09-701-623C-3

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Query Match	45.9%; Score 783; DB 2; Length 313;
Best Local Similarity	49.2%; Pred. No. 3.8e-67;
Matches	150; Conservative 49; Mismatches 100; Indels 6; Gaps 5;

Qy	2	TPPVKILQSSCDGGHPPFTIOLLCLVSGYTTGCTINITWL-EDGQVMDVDLSTASTQIE	60
Db	7	TKPTVDLLHSSCDPNA-FHSTIQLYCFVGHQINDVSIHMLDMDRKIYDTHAQNVLKEE	65
Qy	61	GELASTOSELTLSQKHWLSDRTVTCVYQGHTFEDSTKCCADSNPRGVSAYLSRSPFD	120
Db	66	GKLASTYSRLNITQQQMMSESTICKTSGENYWAHTRCSDDEPAGVITYLIPSPLD	125
Qy	121	LFIRKSPITICLVVDLAPSGTIVNLTSRAGKPVNHSTRKEBKQRNGTLTVTSTLTPVGT	180
Db	126	LYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSASORSTKHNATTSITSLPVD	184
Qy	181	RDMEGTGYQCRVTHPHLPALMRSTTKTSGPRAAEVYAFATPEWPGSRDCKTCLACLIQ	240
Db	185	KDMIEGGYQCRVDHPHPKPIVRSITKALGLRSAPEVYVFLPPE-EEKNKRTLTCLIQ	243
Qy	241	NFPEDISVQWLHNEVQLPDARHSTTQPRKTCGSG--FFVFSLEVTRAWEQKDEFICR	298
Db	244	NFFPEDISVQWLQDSKLIPKSHQSTTTPLKTINGSNQRFIFSRLEVTKALMTQKPTCR	303
Qy	299	AVHEA 303	
Db	304	VIHEA 308	

RESULT 15

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US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match          45.8%; Score 781; DB 2; Length 341;
Best Local Similarity 47.8%; Pred. No. 6.6e-67;
Matches 154; Conservative 59; Mismatches 101; Indels 8; Gaps 5;

Qy 3 PPTVKILOSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDQVMD--VDLSTASTTQE 60
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Db 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAENLFYYTTRPKREG 81
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Qy 61 GELASTQSELTLISQKHLSDRTYTCQVTVQGHTEPDTKCADSNPRGVSAYLSRPSPPD 120
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Db 82 GQTFSLQSEVNITQQWSSNTYTCHVKHNGSIFEDSAQKCSDDTDPKGISAYILPPTPQD 141
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Qy 121 LFIKSPRTITCLVVDLAPSKGTVNLTWGRAGKPVNHSRKEEKQKRNGLTIVTSTLPVGT 180
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Db 142 LFKVKVPTIGCLIVDLA-SAENVKVTWSRGSGPVNPSLVVKEQYNGTFTVTSHPVNT 200
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Qy 181 RDWIEGETYQCRVTHPHLPRLMRSTTKTSGPRAAPEVYAP-ATPEWFGSRDKRTLACLI 239
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Db 201 DDWIEGDTYTCRLSPDMPVPLIRTISKAPGKRLAPEVYMLPPSPPEETGT--TRTVTCLI 258
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Qy 240 QNFMPEDISVOLHNEVOLPDARHSTTTPRKTKGS--GFFVFSRLVTRAEWEOKDEFIC 297
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Db 259 RGFPSEISVQVLFNNEEDHTGHHHTTRPQKHGTDPSFFLYSRMLVNKSIWEKGNLVTC 318
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Qy 298 RAVHEAASPSTQTVQRAVSNPG 319
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Db 319 RVVHEALPGSRTLKSLHYSAG 340
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
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Job time : 39.2609 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:56:45 ; Search time 133.913 Seconds
(without alignments)
998.449 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVKILQSSCDGGGHP.....HEAASPSQTVQRAVSVNPGK 320

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

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2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pap.*
3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pap.*
4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1707	100.0	323	3	US-09-949-375A-4
5	1707	100.0	323	3	US-09-949-375A-6
6	1707	100.0	323	4	US-10-363-954A-2
7	1707	100.0	323	4	US-10-363-954A-4
8	1707	100.0	323	4	US-10-363-954A-6
9	1707	100.0	327	5	US-10-627-556-224
10	1707	100.0	331	3	US-09-401-636-1
11	1707	100.0	331	4	US-10-176-664-1
12	1707	100.0	331	4	US-10-207-655-329
13	1707	100.0	331	4	US-10-673-594-1
14	1707	100.0	331	5	US-10-627-556-97
15	1707	100.0	331	5	US-10-627-556-174
16	1707	100.0	427	3	US-09-847-208-5
17	1707	100.0	427	4	US-10-000-439-5
18	1707	100.0	428	3	US-09-916-230-1
19	1707	100.0	428	3	US-09-949-375A-1
20	1707	100.0	428	4	US-10-047-542-60
21	1707	100.0	428	4	US-10-363-954A-1
22	1707	100.0	569	3	US-09-847-208-7
23	1707	100.0	569	4	US-10-000-439-7
24	1707	100.0	574	4	US-10-047-542-45
25	1707	100.0	574	4	US-10-214-524-37
26	1707	100.0	574	4	US-10-050-902-176
27	1707	100.0	574	4	US-10-050-898-176

28	1707	100.0	586	5	US-10-627-556-384	Sequence 384, App
29	1707	100.0	592	4	US-10-207-655-334	Sequence 334, App
30	1707	100.0	592	5	US-10-627-556-129	Sequence 129, App
31	1707	100.0	593	5	US-10-627-556-248	Sequence 248, App
32	1707	100.0	635	5	US-10-627-556-176	Sequence 176, App
33	1707	100.0	648	5	US-10-627-556-180	Sequence 180, App
34	1707	100.0	648	5	US-10-627-556-184	Sequence 184, App
35	1696	99.4	336	3	US-09-949-375A-8	Sequence 8, Appli
36	1696	99.4	336	4	US-10-363-954A-8	Sequence 8, Appli
37	1696	99.4	441	3	US-09-949-375A-7	Sequence 7, Appli
38	1696	99.4	441	4	US-10-363-954A-7	Sequence 7, Appli
39	1695.5	99.3	497	5	US-10-872-932A-35	Sequence 35, Appl
40	1695.5	99.3	497	5	US-10-810-881A-34	Sequence 34, Appl
41	1695.5	99.3	497	5	US-10-981-936-34	Sequence 34, Appl
42	1671	97.9	330	3	US-09-949-375A-10	Sequence 10, Appl
43	1671	97.9	330	4	US-10-363-954A-10	Sequence 10, Appl
44	1649	96.6	347	4	US-10-152-190-13	Sequence 13, Appl
45	1644.5	96.3	426	4	US-10-214-524-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-09-847-208-6

; Sequence 6, Application US/09847208

; Publication No. US20030082190A1

; GENERAL INFORMATION:

; APPLICANT: Saxon, Andrew

; APPLICANT: Zhang, Ke

; APPLICANT: Zhu, Daocheng

; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES

; FILE REFERENCE: UC67.002A

; CURRENT APPLICATION NUMBER: US/09/847,208

; CURRENT FILING DATE: 2001-05-01

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-847-208-6

Query Match Similarity 100.0%; Score 1707; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.4e-127; Mismatches 0; Indels 0; Gaps 0;
Matches 320; Conservative 0;

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Db	1	FTPTVKILQSSCDGGGHPPTIQLCLIVSGYTPGTINITWLEDQVMDVLDLSTASTTQE	60
Qy	61	GELASTQSELTLQKHWLSDRITYTCQVITYQHTFEDSTKCADSNPRGVAYLSRPSPPD	120
Db	61	GELASTQSELTLQKHWLSDRITYTCQVITYQHTFEDSTKCADSNPRGVAYLSRPSPPD	120
Qy	121	LFIRKSPITICLVVDLAPSKGTVNLWTSRASKPVNHSTRKEKORNGTLTWTSTLPVGT	180
Db	121	LFIRKSPITICLVVDLAPSKGTVNLWTSRASKPVNHSTRKEKORNGTLTWTSTLPVGT	180
Qy	181	RDWTEGETYQCRVTHPHLPRALMESTTKTSGPRAAPEVYAFATPEWPGSRDKRTIACLIQ	240
Db	181	RDWTEGETYQCRVTHPHLPRALMESTTKTSGPRAAPEVYAFATPEWPGSRDKRTIACLIQ	240
Qy	241	NFMPEDISVQMLHNEVQLPDARHSTTPQRTKSGGFFVFSRLVETRAWEQKDEFCRAV	300
Db	241	NFMPEDISVQMLHNEVQLPDARHSTTPQRTKSGGFFVFSRLVETRAWEQKDEFCRAV	300
Qy	301	HEAASPSQTVQRAVSVNPGK	320
Db	301	HEAASPSQTVQRAVSVNPGK	320

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RESULT 2
US-10-000-439-6
; Sequence 6, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-6

Query Match      100.0%; Score 1707; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 60
Db 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 60
QY 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120
QY 121 LFIKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
Db 121 LFIKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
QY 181 RDWIEGTQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 240
Db 181 RDWIEGTQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 240
QY 241 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300
Db 241 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300
QY 301 HEAASPQTQVQRAVSVNPGK 320
Db 301 HEAASPQTQVQRAVSVNPGK 320

RESULT 3
US-09-949-375A-2
; Sequence 2, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human IgE heavy chain C2 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)

; OTHER INFORMATION: Human IgE heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human IgE heavy chain C4 domain
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (210)..(218)
; OTHER INFORMATION: Epitope including C3C4 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (196)..(206)
; OTHER INFORMATION: Epitope in FG loop
US-09-949-375A-2

Query Match      100.0%; Score 1707; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 60
Db 4 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 63
QY 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db 64 GELASTQSELTLSQKHLSDRTYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 123
QY 121 LFIKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
Db 124 LFIKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKQKNGTLTVTSTLPVGT 183
QY 181 RDWIEGTQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 240
Db 184 RDWIEGTQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 243
QY 241 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300
Db 244 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 303
QY 301 HEAASPQTQVQRAVSVNPGK 320
Db 304 HEAASPQTQVQRAVSVNPGK 323

RESULT 4
US-09-949-375A-4
; Sequence 4, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
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	CURRENT FILING DATE: 2002-01-18	
	NUMBER OF SEQ ID NOS: 38	
	SOFTWARE: PatentIn version 3.1	
	SEQ ID NO 4	
	LENGTH: 323	
	TYPE: PRT	
	ORGANISM: Artificial Sequence	
	FEATURE:	
	OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.	
	US-09-949-375A-4	
	Query Match	100.0%; Score 1707; DB 3; Length 323;
	Best Local Similarity	100.0%; Pred. No. 2.4e-127;
	Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FTPTVKILQSSCDGGHPPPTIQLCLVSGVTGPGTINITWLEDGVMDVDLSTASTTQE 60	
DB	4 FTPTVKILQSSCDGGHPPPTIQLCLVSGVTGPGTINITWLEDGVMDVDLSTASTTQE 63	
QY	61 GELASTQSELTLSQKHWLSDRTYTCCVTVQGHTFEDSTKKCADSNPRGVSAVLSRSPFD 120	
DB	64 GELASTQSELTLSQKHWLSDRTYTCCVTVQGHTFEDSTKKCADSNPRGVSAVLSRSPFD 123	
QY	121 LFIKSPPTICLVLDAPSKGTNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 180	
DB	124 LFIKSPPTICLVLDAPSKGTNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 183	
QY	181 RWIEGETYQCVRTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240	
DB	184 RWIEGETYQCVRTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243	
QY	241 NFMPEDISVQWLHNVEQLPDARHSITTPRKTKGSGFFVFSLRVLEVTAEWEQKDFICRAV 300	
DB	244 NFMPEDISVQWLHNVEQLPDARHSITTPRKTKGSGFFVFSLRVLEVTAEWEQKDFICRAV 303	
QY	301 HEAAASPSQTAVRSVNPCK 320	
DB	304 HEAAASPSQTAVRSVNPCK 323	
	RESULT 5	
	US-09-949-375A-6	
	; Sequence 6, Application US/09949375A	
	; Patent No. US20020172673A1	
	; GENERAL INFORMATION:	
	; APPLICANT: KLYSNER, Steen et al.	
	; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE	
	; FILE REFERENCE: 3631-011P	
	; CURRENT APPLICATION NUMBER: US/09/949,375A	
	; CURRENT FILING DATE: 2002-01-18	
	; NUMBER OF SEQ ID NOS: 38	
	; SOFTWARE: PatentIn version 3.1	
	; SEQ ID NO 6	
	LENGTH: 323	
	TYPE: PRT	
	ORGANISM: Artificial Sequence	
	FEATURE:	
	OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.	
	US-09-949-375A-6	
	Query Match	100.0%; Score 1707; DB 3; Length 323;
	Best Local Similarity	100.0%; Pred. No. 2.4e-127;
	Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FTPTVKILQSSCDGGHPPPTIQLCLVSGVTGPGTINITWLEDGVMDVDLSTASTTQE 60	
DB	4 FTPTVKILQSSCDGGHPPPTIQLCLVSGVTGPGTINITWLEDGVMDVDLSTASTTQE 63	
QY	61 GELASTQSELTLSQKHWLSDRTYTCCVTVQGHTFEDSTKKCADSNPRGVSAVLSRSPFD 120	
DB	64 GELASTQSELTLSQKHWLSDRTYTCCVTVQGHTFEDSTKKCADSNPRGVSAVLSRSPFD 123	
	121 LFIKSPPTICLVLDAPSKGTNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 180	
	124 LFIKSPPTICLVLDAPSKGTNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVGT 183	
	181 RWIEGETYQCVRTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240	
	184 RWIEGETYQCVRTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243	
	241 NFMPEDISVQWLHNVEQLPDARHSITTPRKTKGSGFFVFSLRVLEVTAEWEQKDFICRAV 300	
	244 NFMPEDISVQWLHNVEQLPDARHSITTPRKTKGSGFFVFSLRVLEVTAEWEQKDFICRAV 303	
	301 HEAAASPSQTAVRSVNPCK 320	
	304 HEAAASPSQTAVRSVNPCK 323	
	RESULT 6	
	US-10-363-954A-2	
	; Sequence 2, Application US/10363954A	
	; Publication No. US20040156838A1	
	; GENERAL INFORMATION:	
	; APPLICANT: KLYSNER, Steen et al.	
	; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE	
	; FILE REFERENCE: 4614-0115P	
	; CURRENT APPLICATION NUMBER: US/10/363,954A	
	; CURRENT FILING DATE: 2003-03-06	
	; PRIOR APPLICATION NUMBER: US 60/232,831	
	; PRIOR FILING DATE: 2000-09-15	
	; PRIOR APPLICATION NUMBER: DK PA 2000 01326	
	; PRIOR FILING DATE: 2000-09-06	
	; NUMBER OF SEQ ID NOS: 38	
	; SOFTWARE: PatentIn version 3.1	
	; SEQ ID NO 2	
	LENGTH: 323	
	TYPE: PRT	
	ORGANISM: Homo sapiens	
	FEATURE:	
	NAME/KEY: DOMAIN	
	LOCATION: (8)..(103)	
	OTHER INFORMATION: Human IgE heavy chain C2 domain	
	FEATURE:	
	NAME/KEY: DOMAIN	
	LOCATION: (112)..(211)	
	OTHER INFORMATION: Human IgB heavy chain C3 domain	
	FEATURE:	
	NAME/KEY: DOMAIN	
	LOCATION: (216)..(317)	
	OTHER INFORMATION: Human IgE heavy chain C4 domain	
	FEATURE:	
	NAME/KEY: MISC FEATURE	
	LOCATION: (104)..(111)	
	OTHER INFORMATION: Linker between domains C2 and C3	
	FEATURE:	
	NAME/KEY: MISC FEATURE	
	LOCATION: (212)..(215)	
	OTHER INFORMATION: Linker between domains C3 and C4	
	FEATURE:	
	NAME/KEY: MISC FEATURE	
	LOCATION: (100)..(114)	
	OTHER INFORMATION: Epitope including C2C3 linker	
	FEATURE:	
	NAME/KEY: MISC FEATURE	
	LOCATION: (210)..(218)	
	OTHER INFORMATION: Epitope including C3C4 linker	
	FEATURE:	
	NAME/KEY: MISC FEATURE	
	LOCATION: (139)..(145)	
	OTHER INFORMATION: Epitope in BC loop	
	FEATURE:	
	NAME/KEY: MISC FEATURE	
	LOCATION: (167)..(175)	
	OTHER INFORMATION: Epitope in DE loop	
	FEATURE:	

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Db	64	GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 123
Qy	121	LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQNGTLTVTSTLPVGT 180
Db	124	LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQNGTLTVTSTLPVGT 183
Qy	181	RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTTLACLIQ 240
Db	184	RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTTLACLIQ 243
Qy	241	NMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 300
Db	244	NMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 303
Qy	301	HEAASPSQTVQRAVSNPGK 320
Db	304	HEAASPSQTVQRAVSNPGK 323
RESULT 8		
US-10-363-954A-6		
Sequence 6, Application US/10363954A		
Publication No. US20040156838A1		
GENERAL INFORMATION:		
APPLICANT: KLYSNER, Steen et al.		
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE		
FILE REFERENCE: 4614-0115P		
CURRENT APPLICATION NUMBER: US/10/363,954A		
CURRENT FILING DATE: 2003-03-06		
PRIOR APPLICATION NUMBER: US 60/232,831		
PRIOR FILING DATE: 2000-09-15		
PRIOR APPLICATION NUMBER: DK PA 2000 01326		
PRIOR FILING DATE: 2000-09-06		
NUMBER OF SEQ ID NOS: 38		
SOFTWARE: Patentin version 3.1		
SEQ ID NO 6		
LENGTH: 323		
TYPE: PRT		
ORGANISM: Artificial Sequence		
FEATURE:		
OTHER INFORMATION: Artificial protein sequence optimized for expression in E. coli of human IgE heavy chain fragment spanning C2,		
OTHER INFORMATION: C3, and C4		
US-10-363-954A-6		
Query Match 100.0%; Score 1707; DB 4; Length 323;		
Best Local Similarity 100.0%; Pred. No. 2.4e-127;		
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	FTPTVKILQSSCDGGGHPPTIQLCLVSGYPTGTTINITWLEDGQVMDVDLSTASTTQE 60
Db	4	FTPTVKILQSSCDGGGHPPTIQLCLVSGYPTGTTINITWLEDGQVMDVDLSTASTTQE 63
Qy	61	GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db	64	GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 123
Qy	121	LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQNGTLTVTSTLPVGT 180
Db	124	LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQNGTLTVTSTLPVGT 183
Qy	181	RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTTLACLIQ 240
Db	184	RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTTLACLIQ 243
Qy	241	NMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 300
Db	244	NMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 303
Qy	301	HEAASPSQTVQRAVSNPGK 320
Db	304	HEAASPSQTVQRAVSNPGK 323


```
RESULT 9
US-10-627-556-224
; Sequence 224, Application US/10627556
; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 224
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-10-627-556-224

Query Match 100.0%; Score 1707; DB 5; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGPTINITWLEDQVMDVLDLSTASTTQE 60
Db 8 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGPTINITWLEDQVMDVLDLSTASTTQE 67

Qy 61 GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 120
Db 68 GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 127

Qy 121 LFIKSPITICLVVDLAPSKGTVNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 180
Db 128 LFIKSPITICLVVDLAPSKGTVNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 187

Qy 181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 188 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 300
Db 248 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 307

Qy 301 HEAASPSQTQRAVSNPGK 320
Db 308 HEAASPSQTQRAVSNPGK 327

RESULT 10
US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1

Query Match 100.0%; Score 1707; DB 3; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGPTINITWLEDQVMDVLDLSTASTTQE 60
Db 12 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGPTINITWLEDQVMDVLDLSTASTTQE 71

Qy 61 GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 120
Db 72 GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 131

Qy 121 LFIKSPITICLVVDLAPSKGTVNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 180
Db 132 LFIKSPITICLVVDLAPSKGTVNLTWSRASKPVNHSRKEEKORNGTLTSTLPVGT 191

Qy 181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 192 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 251

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 300
Db 252 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 311

Qy 301 HEAASPSQTQRAVSNPGK 320
Db 312 HEAASPSQTQRAVSNPGK 331

RESULT 11
US-10-176-664-1
; Sequence 1, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-1

Query Match 100.0%; Score 1707; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGPTINITWLEDQVMDVLDLSTASTTQE 60
Db 12 FTPPTVKILQSSCDGGGHPPTIQLCLVSGVTGPTINITWLEDQVMDVLDLSTASTTQE 71

Qy 61 GELASTQSELTLSQKHWSLDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 120
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Db 72 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 131
QY 121 LFRKSPPTITCLVVDLAPSKGTVNLTWASRAGKPVNHSRKEKQKNGTLTVTSTLTPVGT 180
Db 132 LFRKSPPTITCLVVDLAPSKGTVNLTWASRAGKPVNHSRKEKQKNGTLTVTSTLTPVGT 191
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTGSPRAAPEVAFATPEWPGSRDKETLACLQ 240
Db 192 RDWIEGETYQCRVTHPHLPALMRSTTKTGSPRAAPEVAFATPEWPGSRDKETLACLQ 251
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 300
Db 252 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 311
QY 301 HEAASPSQTVQRAVSNPGK 320
Db 312 HEAASPSQTVQRAVSNPGK 331

RESULT 12
US-10-207-655-329
; Sequence 329, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 329
; TYPE: PRT
; LENGTH: 331
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-329

Query Match 100.0%; Score 1707; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60
Db 8 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 67
QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120
Db 68 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 127
QY 121 LFRKSPPTITCLVVDLAPSKGTVNLTWASRAGKPVNHSRKEKQKNGTLTVTSTLTPVGT 180
Db 128 LFRKSPPTITCLVVDLAPSKGTVNLTWASRAGKPVNHSRKEKQKNGTLTVTSTLTPVGT 187
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTGSPRAAPEVAFATPEWPGSRDKETLACLQ 240
Db 188 RDWIEGETYQCRVTHPHLPALMRSTTKTGSPRAAPEVAFATPEWPGSRDKETLACLQ 247
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 300
Db 248 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 307
QY 301 HEAASPSQTVQRAVSNPGK 320
Db 308 HEAASPSQTVQRAVSNPGK 327

RESULT 13
US-10-673-594-1
; Sequence 1, Application US/10673594
; Publication No. US20040076625A1

; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-1

Query Match 100.0%; Score 1707; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60
Db 12 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 71
QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120
Db 72 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 131
QY 121 LFRKSPPTITCLVVDLAPSKGTVNLTWASRAGKPVNHSRKEKQKNGTLTVTSTLTPVGT 180
Db 132 LFRKSPPTITCLVVDLAPSKGTVNLTWASRAGKPVNHSRKEKQKNGTLTVTSTLTPVGT 191
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTGSPRAAPEVAFATPEWPGSRDKETLACLQ 240
Db 192 RDWIEGETYQCRVTHPHLPALMRSTTKTGSPRAAPEVAFATPEWPGSRDKETLACLQ 251
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 300
Db 252 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 311
QY 301 HEAASPSQTVQRAVSNPGK 320
Db 312 HEAASPSQTVQRAVSNPGK 331

RESULT 14
US-10-627-556-97
; Sequence 97, Application US/10627556
; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 331

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-556-97

Query Match      100.0%; Score 1707; DB 5; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTGTTINITWLEDCQVMDVLDLSTASTQOE 60
Db 8 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTGTTINITWLEDCQVMDVLDLSTASTQOE 67

Qy 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSFFD 120
Db 68 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSFFD 127

Qy 121 LFIKSPITITCLVVDLAPSKGTVNLTWASRSGKPVNHSRKEEKQKQNGTLTFTSTLPVGT 180
Db 128 LFIKSPITITCLVVDLAPSKGTVNLTWASRSGKPVNHSRKEEKQKQNGTLTFTSTLPVGT 187

Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 188 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247

Qy 241 NFMPEDISVQWLHNEVOLPDARHSTTQPRKTGSGFFVFSRLEVTVAEWEQKDEFICRAV 300
Db 248 NFMPEDISVQWLHNEVOLPDARHSTTQPRKTGSGFFVFSRLEVTVAEWEQKDEFICRAV 307

Qy 301 HEAASPSQTVQRAVSVNPGK 320
Db 308 HEAASPSQTVQRAVSVNPGK 327

Search completed: November 30, 2005, 01:16:49
Job time : 134.913 secs
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RESULT 15
US-10-627-556-174
; Sequence 174, Application US/10627556
; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-556-174

Query Match      100.0%; Score 1707; DB 5; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTGTTINITWLEDCQVMDVLDLSTASTQOE 60
Db 8 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTGTTINITWLEDCQVMDVLDLSTASTQOE 67

Qy 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSFFD 120
Db 68 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSFFD 127
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2005, 01:10:40 ; Search time 6.37681 Seconds
(without alignments)
152.100 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVKILQSSCDGGGHP.....HEAASPQTQVRASVNVNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US10 NEW PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06 NEW PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07 NEW PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US08 NEW PUB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09 NEW PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11 NEW PUB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60 NEW PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1701	99.6	1 US-10-723-207-1	Sequence 1, Appli
2	895.5	52.5	1 US-10-723-207-2	Sequence 2, Appli
3	783	45.9	1 US-10-723-207-3	Sequence 3, Appli
4	691.5	40.5	1 US-10-723-207-4	Sequence 4, Appli
5	425	24.9	7 US-11-144-248-45	Sequence 45, Appl
6	425	24.9	7 US-11-144-248-46	Sequence 46, Appl
7	425	24.9	7 US-11-144-248-49	Sequence 49, Appl
8	425	24.9	7 US-11-144-248-50	Sequence 50, Appl
9	422	24.7	7 US-11-025-712-12	Sequence 12, Appl
10	419	24.5	7 US-11-022-289-6	Sequence 6, Appli
11	416	24.4	7 US-11-144-248-28	Sequence 28, Appl
12	416	24.4	7 US-11-022-289-7	Sequence 7, Appli
13	416	24.4	7 US-11-022-289-8	Sequence 8, Appli
14	414.5	24.3	7 US-11-022-289-3	Sequence 3, Appli
15	414	24.3	7 US-10-723-207-40	Sequence 40, Appl
16	414	24.3	7 US-11-022-289-2	Sequence 2, Appli
17	413	24.2	7 US-11-022-289-4	Sequence 4, Appli
18	413	24.2	7 US-11-022-289-5	Sequence 5, Appli
19	399	23.4	7 US-11-172-320-6	Sequence 6, Appli
20	397.5	23.3	7 US-11-022-289-11	Sequence 11, Appl
21	397	23.3	7 US-11-174-186-41	Sequence 41, Appl
22	394.5	23.1	7 US-11-022-289-1	Sequence 1, Appli
23	394.5	23.1	7 US-11-022-289-10	Sequence 10, Appl
24	394	23.1	7 US-10-723-207-31	Sequence 31, Appl
25	376.5	22.1	7 US-11-016-503-10	Sequence 10, Appl

Sequence 6, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 12, Appli
Sequence 17, Appli
Sequence 390, App
Sequence 11, Appli
Sequence 2, Appli
Sequence 389, App
Sequence 14, Appli
Sequence 18, Appli
Sequence 9, Appli
Sequence 30, Appli
Sequence 4, Appli
Sequence 20, Appli
Sequence 22, Appli
Sequence 16, Appli

26 375.5 22.0 452 7 US-11-016-503-6
27 375.5 22.0 462 7 US-11-016-503-8
28 375.5 22.0 557 7 US-11-016-503-4
29 375.5 22.0 567 7 US-11-016-503-2
30 370.5 21.7 458 7 US-11-016-503-16
31 366 21.4 458 7 US-11-016-503-12
32 358 21.0 455 7 US-11-016-503-14
33 355 20.8 430 7 US-11-016-503-17
34 352 20.6 459 1 US-10-949-720-390
35 352 20.6 489 1 US-10-835-475-11
36 352 20.6 514 1 US-10-835-475-2
37 352 20.6 771 1 US-10-949-720-389
38 349 20.4 227 7 US-11-008-727-18
39 349 20.4 531 7 US-11-008-727-18
40 334.5 19.6 353 7 US-11-022-289-9
41 330 19.3 64 1 US-10-723-207-30
42 327.5 19.2 236 7 US-11-008-727-4
43 327.5 19.2 470 7 US-11-008-727-20
44 327.5 19.2 476 7 US-11-008-727-22
45 327.5 19.2 509 7 US-11-008-727-16

ALIGNMENTS

RESULT 1

US-10-723-207-1

; Sequence 1, Application US/10723207

; Publication No. US20050250934A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; APPLICANT: Walfield, Alan M.

; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

; TITLE OF INVENTION: ALLERGY

; FILE REFERENCE: 1151-4153US2

; CURRENT APPLICATION NUMBER: US/10/723.207

; CURRENT FILING DATE: 2003-11-24

; PRIOR APPLICATION NUMBER: 09/701,623

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US99/13959

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 09/100,287

; PRIOR FILING DATE: 1998-06-20

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 325

; TYPE: PRT

; ORGANISM: HUMAN

; FEATURE:

; OTHER INFORMATION: CH2CH3 of human Ige

; PUBLICATION INFORMATION:

; AUTHORS: Dorrington,

; AUTHORS: Bennich,

; JOURNAL: Immunology

; VOLUME: 41

; PAGES: 3-25

; DATE: 1978

US-10-723-207-1

Query Match 99.6%; Score 1701; DB 1; Length 325;

Best Local Similarity 99.4%; Pred. No. 1.4e-111;

Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTPGTINITWLEDQVMDVLDLSTATTQE 60

Db 6 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTPGTINITWLEDQVMDVLDLSTATTQE 65

Qy 61 GELASTQSELTLSQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRPSPPD 120

Db 66 GELASTQSELTLSQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRPSPPD 125

Qy 121 LFIKSPITITCLVLDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180

Db 126 LFIKSGPTTICLVVDLAPSGVTNLTWSRAGKPVNHSRKKEQRNGTLTSTLPVGT 185
Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 186 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245
Qy 241 NFWPDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLRLEVTRAWEQKDEFTICRAV 300
Db 246 NFWPDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLRLEVTRAWEQKDEFTICRAV 305
Qy 301 HEAPSOTVQRAVSNPGK 320
Db 306 HEAPSOTVQRAVSNPGK 325
RESULT 2
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 1151-4153US2
; CURRENT FILING DATE: 2003-11-24
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IGE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2
Query Match 52.5%; Score 895.5; DB 1; Length 312;
Best Local Similarity 55.1%; Pred. No. 5.2e-56;
Matches 172; Conservative 48; Mismatches 83; Indels 9; Gaps 5;
Qy 1 FTPPTVKILOSCDGGGHPPTTQLLCLVSGYTPGTINITWLBDGQ-VMDVDLSTASTTQ 59
Db 6 FIPPTVKLHFSSNPNVGDTHHTIQLLCLISGYVPGDMEVILVDDGQKATNIFFFYATPGTK 65
Qy 60 EGEASTQSELTLSQKHLSDRTYTCQVTVQGHTEFEDSTKKCADSNPRGVSAYLSRSPPF 119
Db 66 EGNVTSTHSELNITQGWVSQKTYTC---QGFTFKDEARKKCSDEPRGVTISLSPSPSL 121
Qy 120 DLFIKSGPTTICLVVDLAPSGVTNLTWSRAGKPVNHSRKKEQRNGTLTSTLPVGT 179
Db 122 DLYVHKAPKTCILVVDLATEWG-MNLTWYRESKEPVNPGPLNKKDHENGITVTSTLPVN 180
Qy 180 TRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATP-BWPGSRDKRTLACLI 238
Db 181 TNDWIEGETYQCRVTHPHLPKDIIVRSIAKAPGKRAPPDVLFLFPPEEQGTOKDRTVLTCL 240
Qy 239 IQNFWPDISVQWLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLRLEVTRAWEQKDEFTI 296
Db 241 IQNFWPDISVQWLHNEVQLPDARHSTTQPRKTKGS--GFFVFSRLRLEVTRAWEQKDEFTI 300

Qy 297 CRAVHEAASPSQ 308
Db 301 CQWHEALSGSR 312
RESULT 3
US-10-723-207-3
; Sequence 3, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 1151-4153US2
; CURRENT FILING DATE: 2003-11-24
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 313
; TYPE: PRT
; ORGANISM: RAT
; FEATURE:
; OTHER INFORMATION: CH2CH3 of rat IGE
; PUBLICATION INFORMATION:
; AUTHORS: Dorrington,
; JOURNAL: Immunology
; VOLUME: 41
; PAGES: 3-25
; DATE: 1978
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; PUBLICATION INFORMATION:
; AUTHORS: Steen,
; JOURNAL: J. Mol. Biol.
; VOLUME: 177
; PAGES: 19-32
; DATE: 1984
; PUBLICATION INFORMATION:
; AUTHORS: Ishida,
; JOURNAL: EMBO J.
; VOLUME: 1
; PAGES: 1117-1123
; DATE: 1982
US-10-723-207-3
Query Match 45.9%; Score 783; DB 1; Length 313;
Best Local Similarity 49.2%; Pred. No. 3.1e-48;
Matches 150; Conservative 49; Mismatches 100; Indels 6; Gaps 5;
Qy 2 TPPTVKILOSCDGGGHPPTTQLLCLVSGYTPGTINITWL-BDQVMDVDLSTASTTQ 60
Db 7 TKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHQNDVSIHLMDRDKIYDTHAQNVLIKEE 65
Qy 61 GEIASTQSELTLSQKHLSDRTYTCQVTVQGHTEFEDSTKKCADSNPRGVSAYLSRSPPF 120
Db 66 GKLAITSYRLNITQQQWMESEFTTCKTSQGENYWAHTRCSDDEPRGVITVLIIPSPLD 125
Qy 121 LFIKSGPTTICLVVDLAPSGVTNLTWSRAGKPVNHSRKKEQRNGTLTSTLPVGT 180

Db 126 LYENGTPKLTCLVLDL-ESEENITVWVRERKKSIGSASORSTKHNATTSTISILPVD 184
Qy 181 RDWIEGETYQCRVTHPLPRALMSTYKTSGRAPAEVAFATPEWPGSRDKRTLACLIQ 240
Db 185 KDWIEGEGYQCRVDPHPKPIVRSITKALGLRSAPEVYVFLPPE-BEEKNKRTLTLIQ 243
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTORPKTKGSG--FFVFSRLVTRAEWEQKDEFICR 298
Db 244 NFFEDISVQWLQSLKPLPKSQHSTTTLKNGSNQRFIFSRLEVTKALWTQTKQFCR 303
Qy 299 AVHEA 303
Db 304 VIHEA 308

RESULT 4
US-10-723-207-4
; Sequence 4, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: MOUSE
; FEATURE:
; OTHER INFORMATION: CH2CH3 of mouse Ige
US-10-723-207-4

Query Match 40.5%; Score 691.5; DB 1; Length 313;
Best Local Similarity 46.4%; Pred. No. 6.3e-42;
Matches 136; Conservative 51; Mismatches 101; Indels 5; Gaps 5;
Qy 13 CDGGHFPPTIQLCLVSGYTPGTINITWL-EDGOVMDVDLSTASTOGBELASTQSELT 71
Db 19 CDPNA-FHSTIQLYCFIYGHILNDVSVWLMDDREITDTLAQTVLKKEGKLASTCSKLN 77
Qy 72 LSQKHLSDRTYTCQVYQGHTEFSDTKKCADSNPRGVSAYLSRSPFDFLRKSPITTC 131
Db 78 ITEQWMSESTTCRVTSQGCYLAHTRCPDHEPRGAIITYLIPSPDLQNGAPKLTCL 137
Qy 132 LVVDLAPSKGTNLTWSRASKGPNVHSTRKEQKNGILTVSTLTPVGTDRWIEGETYQC 191
Db 138 LVVDLESEK-NVNVITWNOEKTSVSASQWYTKHNNATTSTISILPVAKWIEGYGYQC 196
Qy 192 RVTHPLPRALMRSTTKTSGRAPAEVAFATPEWPGSRDKRTLACLIQNFMPEDISVQW 251
Db 197 IVDRPDPFKPIVRSITKTPGQSAPEVYVFPPE-BESDKKTLTCLIQNFFPEDIQW 255
Qy 252 LHNEVQLPDARHSTTORPKTKGS-GFFVFSRLVTRAEWEQKDEFICRAVHEA 303
Db 256 LGDGKLSNSQHSSTTTLKSNQNGQFFIFSRLEVAKTLWTQKQTCQVHEA 308

RESULT 5
US-11-144-248-45
; Sequence 45, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:

; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-45
Query Match 24.9%; Score 425; DB 7; Length 470;
Best Local Similarity 31.3%; Pred. No. 2.3e-23;
Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;
Qy 5 TVKILQSSCDGGHFP-----PTIQLCLVSGYTPGTINITWLEDGOVMDVDLST 54
Db 139 TVTVSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFFPEPVTVSW-NSGALTSGVHTF 197
Qy 55 ASTTQEGELASTQSELTLQKHLSDRTYTCQVYQ-GHTEPDST---KKCADSNP----- 106
Db 198 PAVLQSSGLYSLSSVTVVPSNF-GTQYTCNVDPKPSNTKVDKTVKCKCCVECPCPAP 256
Qy 107 --RGVSAYLSRSPFD-LFIRKSPITCLVDLAPSKGTNLTWSRASKGPNVHSTRKEE 163
Db 257 PVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQFNMYVDGVVHNAKTKPRE 316
Qy 164 KORNGTLTVTSTPLVGTDRDTEGETYQCRVTHPLPRALMSTTKTSGRAPAEVYAFAT 223
Db 317 EQFNSTFRVSVLTVVHODWLNQKEYCKVSKNGLPAPIEKTIISKTQGPQVYTL-- 374
Qy 224 PEWPGSRDKRT-----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTORPKTKSGPFFV 278
Db 375 ---PPSREEMTKNQVSLTCLVKGFVPSDIAVEWESN--GQPENNYKTTTPMLDSDGSFPL 429
Qy 279 FSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSNPGK 320
Db 430 YSKLTVDKSRWQGNVFCVSMHEALHNHYT-QKSLSLSPGK 470

RESULT 6
US-11-144-248-46
; Sequence 46, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46

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; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-46

Query Match      24.9%; Score 425; DB 7; Length 470;
Best Local Similarity 31.3%; Pred. No. 2.3e-23;
Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;

Qy 5 TVKILQSSCDGGGHP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLDST 54
Db 139 TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW-NSGALTSGVHTF 197
Qy 55 ASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQ-GHTFEDST---KKCADSNP-----106
Db 198 PAVLQSSGLYSLSSVTVPSNFGTQYTCNVDHKPSNTKVDKTVVERKCCVCEPCPCAP 256

Qy 107 --RGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEE 163
Db 257 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNKTKPRE 316
Qy 164 KORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT 223
Db 317 EQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISTKGGPREQVYTL-- 374
Qy 224 PEWPGSRDKT-----LACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFV 278
Db 375 ---PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPNENYKTTTPPMLDSGSGFFL 429
Qy 279 FSRLEVTAEWQKDEFCICRAVHEAASPSQTQVRAVSNPGK 320
Db 430 YSKLTVDKSRWQGNVFCSCVMHEALHNHYT--QKSLSLSPGK 470

RESULT 7
US-11-144-248-49
; Sequence 49, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 49
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-49

Query Match      24.9%; Score 425; DB 7; Length 470;
Best Local Similarity 31.3%; Pred. No. 2.3e-23;
Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;

Qy 5 TVKILQSSCDGGGHP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLDST 54
Db 139 TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW-NSGALTSGVHTF 197
Qy 55 ASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQ-GHTFEDST---KKCADSNP-----106
Db 198 PAVLQSSGLYSLSSVTVPSNFGTQYTCNVDHKPSNTKVDKTVVERKCCVCEPCPCAP 256

Qy 107 --RGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEE 163
Db 257 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNKTKPRE 316
Qy 164 KORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT 223
Db 317 EQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISTKGGPREQVYTL-- 374
Qy 224 PEWPGSRDKT-----LACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFV 278
Db 375 ---PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPNENYKTTTPPMLDSGSGFFL 429
Qy 279 FSRLEVTAEWQKDEFCICRAVHEAASPSQTQVRAVSNPGK 320
Db 430 YSKLTVDKSRWQGNVFCSCVMHEALHNHYT--QKSLSLSPGK 470

RESULT 8
US-11-144-248-50
; Sequence 50, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-50

Query Match      24.9%; Score 425; DB 7; Length 473;
Best Local Similarity 31.3%; Pred. No. 2.4e-23;
Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;

Qy 5 TVKILQSSCDGGGHP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLDST 54
Db 142 TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW-NSGALTSGVHTF 200
Qy 55 ASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQ-GHTFEDST---KKCADSNP-----106
Db 201 PAVLQSSGLYSLSSVTVPSNFGTQYTCNVDHKPSNTKVDKTVVERKCCVCEPCPCAP 259
Qy 107 --RGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEE 163
Db 260 PVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNKTKPRE 319
Qy 164 KORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT 223
Db 320 EQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISTKGGPREQVYTL-- 377
Qy 224 PEWPGSRDKT-----LACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFV 278
Db 378 ---PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPNENYKTTTPPMLDSGSGFFL 432
Qy 279 FSRLEVTAEWQKDEFCICRAVHEAASPSQTQVRAVSNPGK 320
Db 433 YSKLTVDKSRWQGNVFCSCVMHEALHNHYT--QKSLSLSPGK 473
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RESULT 9
US-11-025-712-12
; Sequence 12, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
;           Thomas, G. Roger
;           Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/025,712
; FILING DATE: 28-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2003
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-Dec-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-Feb-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-Jan-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-Jan-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;
US-11-025-712-12
Query Match 24.7%; Score 422; DB 7; Length 450;
Best Local Similarity 31.1%; Pred. No. 3.6e-23;
Matches 106; Conservative 61; Mismatches 138; Indels 36; Gaps 11;
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DB 120 VTVSSASTKPSVFPFLAPCSRSTSESTAALGLVKDYFPFPTVSN-NSGALTSGVHTFP 178
QY 56 STTQEGELASTQELTSLQKHWLSDRYTCQVYQ-GHTFEDST---KKCADSNP----- 106
DB 179 AVLQSSGLSLSSVTVTSNFGTQYTCNVDPKPSNTKVDKTKVERKCCVCPCPAPP 237
QY 107 -RGVSAYLSRSPFD-LFRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEEK 164
DB 238 VAGPSVFLFPKPKOTLMISRPEVTCVVDVSHEDPEVQFNWYDGMVHNKTKPREE 297
QY 165 QRNGTLTVTSTLPVGRDMEGETYQCRVTHPLPALMRSTTKSGPRAAPEVYAFATP 224
DB 298 QFNSTFRVSVLTVVHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL--- 354
QY 225 EWPGRDKEK-----LACLIQNFMPEDISVQWLHNEVQLPDARHSITQPRKTKGSGFFVFP 279

RESULT 10
US-11-022-289-6
; Sequence 6, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
;
US-11-022-289-6
Query Match 24.5%; Score 419; DB 7; Length 557;
Best Local Similarity 30.2%; Pred. No. 7.2e-23;
Matches 100; Conservative 57; Mismatches 136; Indels 38; Gaps 9;
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QY 20 PPT-----IQLCLVSGYPTGTINITWLEDGQVMDVLDSTATTQEGELASTQSELT 71
DB 235 PPSRDELTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 294
QY 72 LSQKHWLSDRYTCQVYQ-GHTF-----EDSTKKCADSNP---RGVSAYLSR 115
DB 295 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPKDKTHCTPPSPAPDELGGPSVFLFP 354
QY 116 PSPFD-LFRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTS 174
DB 355 PKPKDTLMISRPEVTCVVDVSHEDPEVKFNWYDGMVHNKTKPREEQYNSTYRVVS 414
QY 175 TLPVGRDMEGETYQCRVTHPLPALMRSTTKSGPRAAPEVYAFATPWPGRDKEK 234
DB 415 VLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSRDEL 469
QY 235 -----LACLIQNFMPEDISVQWLHNEVQLPDARHSITQPRKTKGSGFFVFSRLEVTRAEW 289
DB 470 KNQVSLTCLVKGFYPSDIAVEWESN---GQPNENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 527
QY 290 EKKDFICRAVHEAASPSQTQVRAVSNPGK 320
DB 528 QGQNVFCSCVMHEALHNHYT-QKSLSLSPGK 557

RESULT 11
US-11-144-248-28
; Sequence 28, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:33:18 ; Search time 10 Seconds
(without alignments)
172.462 Million cell updates/sec

Title: US-09-847-208B-7
Perfect score: 3060
Sequence: 1 EPKCDKTHTCPCPAPELL.....HEAASPTQVQRAVNVPGK 569

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
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4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1701	55.6	325	1	US-10-723-207-1
2	1518	49.6	557	7	US-11-022-289-6
3	1513	49.4	551	7	US-11-022-289-8
4	1513	49.4	557	7	US-11-022-289-4
5	1511	49.4	551	7	US-11-022-289-7
6	1511	49.4	557	7	US-11-022-289-5
7	1510	49.3	557	7	US-11-022-289-2
8	1497.5	48.9	548	7	US-11-022-289-3
9	1412.5	46.2	564	7	US-11-022-289-10
10	1225	40.0	330	7	US-11-022-289-11
11	1225	40.0	444	7	US-11-172-320-6
12	1225	40.0	452	7	US-11-016-503-6
13	1225	40.0	459	1	US-10-949-720-390
14	1225	40.0	462	7	US-11-016-503-8
15	1225	40.0	489	1	US-10-835-475-11
16	1225	40.0	514	1	US-10-835-475-2
17	1225	40.0	557	7	US-11-016-503-4
18	1225	40.0	567	7	US-11-016-503-2
19	1225	40.0	567	7	US-11-016-503-10
20	1225	40.0	771	1	US-10-949-720-389
21	1219	39.8	330	7	US-11-022-289-1
22	1219	39.8	579	7	US-11-174-186-41
23	1205.5	39.4	531	7	US-11-008-727-18
24	1195	39.1	455	7	US-11-016-503-14
25	1195	39.1	458	7	US-11-016-503-12

26	1195	39.1	458	7	US-11-016-503-16
27	1189	38.9	227	7	US-11-008-727-14
28	1176	38.4	430	7	US-11-016-503-17
29	1107	36.2	326	7	US-11-144-248-28
30	1107	36.2	470	7	US-11-144-248-45
31	1107	36.2	470	7	US-11-144-248-46
32	1107	36.2	470	7	US-11-144-248-49
33	1107	36.2	473	7	US-11-144-248-50
34	1104	36.1	450	7	US-11-025-712-12
35	896.5	29.3	312	1	US-10-723-207-2
36	785.5	25.7	476	7	US-11-008-727-22
37	784	25.6	313	1	US-10-723-207-3
38	779	25.5	509	7	US-11-008-727-16
39	776	25.4	236	7	US-11-008-727-4
40	776	25.4	470	7	US-11-008-727-20
41	693	22.6	313	1	US-10-723-207-4
42	414	13.5	76	1	US-10-723-207-40
43	394	12.9	76	1	US-10-723-207-31
44	334.5	10.9	353	7	US-11-022-289-9
45	330	10.8	64	1	US-10-723-207-30

ALIGNMENTS

RESULT 1
US-10-723-207-1
; Sequence 1, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Walfield, Alan M.
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723.207
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 325
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: CH2CH3 of human Ige
; PUBLICATION INFORMATION:
; AUTHORS: Dorrington,
; AUTHORS: Bennich,
; JOURNAL: Immunology
; VOLUME: 41
; PAGES: 3-25
; DATE: 1978
US-10-723-207-1

Query Match	55.6%;	Score 1701;	DB 1;	Length 325;
Best Local Similarity	99.4%;	Pred. No. 6.3e-77;		
Matches 318;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
QY	250	FTPTVTVKILQSSCDGGHFPPTIQLCLVSGVTGTTINITWLEDQGVMDVLDLSTATTQE	309	Sequence 16, Appl
Db	6	FTPTVTVKILQSSCDGGHFPPTIQLCLVSGVTGTTINITWLEDQGVMDVLDLSTATTQE	65	Sequence 14, Appl
QY	310	GELASTQSELTLISQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD	369	Sequence 28, Appl
Db	66	GELASTQSELTLISQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD	125	Sequence 45, Appl
QY	370	LFIRKSPITCLVLDLAPSKGTVNLTSRASKPVNHSRKEEKQRNGTLTWTSTLPVGT	429	Sequence 49, Appl

Db 126 LFIKSTITICLVLDLAPSGTGNLTWSRAGKPVNHSIRKEEKQKQNGTLTIVTSTLPVGT 185
Qy 430 RDWIEGTYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSDKRTLACLIQ 489
Db 186 RDWIEGTYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSDKRTLACLIQ 245
Qy 490 NFWPEDIISVQWLHNEVOLPDARHSTTQPRKTKSGGFFVFSRLVTRAWEQKDEFICRAV 549
Db 246 NFWPEDIISVQWLHNEVOLPDARHSTTQPRKTKSGGFFVFSRLVTRAWEQKDEFICRAV 305
Qy 550 HEAASPSQTVQRAVSVNPGK 569
Db 306 HEAASPSQTVQRAVSVNPGK 325
RESULT 2
US-11-022-289-6
; Sequence 6, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-6
Query Match 49.6%; Score 1518; DB 7; Length 557;
Best Local Similarity 53.2%; Pred. No. 6.9e-68;
Matches 306; Conservative 47; Mismatches 100; Indels 122; Gaps 7;
Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGKVEGGGSG 240
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSPGK----- 330
Qy 241 GGGSGGGSGFTPTVKILQSSCDGGGHFPPTIQLCLVSGYTPGTINITWLEDQGVMDVD 300
Db 331 -----DKTHTC----- 330
Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVTYQGHTEFDSSTKKCADSNPRGVSA 360
Db 331 ----- 330
Qy 361 YLSRPSFPD-LFIKSTITICLVLDLAPSGTGNLTWSRAGKPVNHSIRKEEKQKQNGTL 419
Db 351 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTY 410
Qy 420 TVTSTLPVGRDMEIGTYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSR 479
Db 411 RVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSR 465

Qy 480 DKRT-----LACIQNFWPEDIISVQWLHNEVOLPDARHSTTQPRKTKSGGFFVFSRLV 534
Db 466 DELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTPPPVLDSDGDSFFLYSKLTVD 523
Qy 535 RAWEQKQDEFICRAVHEAASPSQTVQRAVSVNPGK 569
Db 524 KSRWQQGNVFCSCVMHEALHNYT-QKSLSPGK 557
RESULT 3
US-11-022-289-8
; Sequence 8, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-8
Query Match 49.4%; Score 1513; DB 7; Length 551;
Best Local Similarity 53.2%; Pred. No. 1.2e-67;
Matches 306; Conservative 47; Mismatches 94; Indels 128; Gaps 8;
Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGKVEGGGSG 240
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSPGK----- 330
Qy 241 GGGSGGGSGFTPTVKILQSSCDGGGHFPPTIQLCLVSGYTPGTINITWLEDQGVMDVD 300
Db 331 -----PPS-----PAPELL----- 339
Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVTYQGHTEFDSSTKKCADSNPRGVSA 360
Db 340 ----- 344
Qy 361 YLSRPSFPD-LFIKSTITICLVLDLAPSGTGNLTWSRAGKPVNHSIRKEEKQKQNGTL 419
Db 345 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTY 404
Qy 420 TVTSTLPVGRDMEIGTYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSR 479
Db 405 RVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSR 459
Qy 480 DKRT-----LACIQNFWPEDIISVQWLHNEVOLPDARHSTTQPRKTKSGGFFVFSRLV 534
Db 460 DELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTPPPVLDSDGDSFFLYSKLTVD 517
Qy 535 RAWEQKQDEFICRAVHEAASPSQTVQRAVSVNPGK 569

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; Sequence 7, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-11-022-289-7

Query Match 49.4%; Score 1513; DB 7; Length 551;
Best Local Similarity 53.2%; Pred. No. 1.2e-67;
Matches 306; Conservative 47; Mismatches 100; Indels 122; Gaps 7;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNVTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIET 120
Db 159 NWYVDGVEVHNVTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIET 218
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSLSPGK 240
Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSLSPGK 330
Qy 241 GGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVD 300
Db 331 -----PP-----C-----PAPELL----- 339
Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCKADSNPRGUSA 360
Db 340 ----- 344
Qy 361 YLSRPSFD-LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTL 419
Db 345 FLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQNSTY 404
Qy 420 TVTSTLPVGRDWTGEGTYQCRVTHPLPALMRSTTKTSGPRAAPEYAFATPEWPGSR 479
Db 405 RVSVSLTVLHODWLNKKEYCKVSNKALPAPIETISKAKGQPREPQVYTL-----PPSR 459
Qy 480 DKRT-----LACLQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKSGGFVFSRLVET 534
Db 460 DELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTPPVLDSDGSGFFLYSKLTVD 517
Qy 535 RAEWEQKDEFICRAVHEAASPSQTQRAVSNPGK 569
Db 518 KSRWQQGNVFCSCVMHEALHNNHYT-QKSLSLSPGK 551

RESULT 6
US-11-022-289-5
; Sequence 5, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; ;

; Sequence 4, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-11-022-289-4

Query Match 49.4%; Score 1513; DB 7; Length 557;
Best Local Similarity 53.2%; Pred. No. 1.2e-67;
Matches 306; Conservative 47; Mismatches 100; Indels 122; Gaps 7;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNVTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIET 120
Db 159 NWYVDGVEVHNVTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIET 218
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSLSPGK 240
Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQKSLSLSPGK 330
Qy 241 GGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVD 300
Db 331 ----- 330
Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCKADSNPRGUSA 360
Db 331 -----DKHT-----SPSPAPPELLGGPSV 350
Qy 361 YLSRPSFD-LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTL 419
Db 351 FLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQNSTY 410
Qy 420 TVTSTLPVGRDWTGEGTYQCRVTHPLPALMRSTTKTSGPRAAPEYAFATPEWPGSR 479
Db 411 RVSVSLTVLHODWLNKKEYCKVSNKALPAPIETISKAKGQPREPQVYTL-----PPSR 465
Qy 480 DKRT-----LACLQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKSGGFVFSRLVET 534
Db 466 DELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTPPVLDSDGSGFFLYSKLTVD 523
Qy 535 RAEWEQKDEFICRAVHEAASPSQTQRAVSNPGK 569
Db 524 KSRWQQGNVFCSCVMHEALHNNHYT-QKSLSLSPGK 557

RESULT 5
US-11-022-289-7
```

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; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-5

Query Match          49.4%; Score 1511; DB 7; Length 557;
Best Local Similarity 53.1%; Pred. No. 1.5e-67;
Matches 306; Conservative 48; Mismatches 98; Indels 124; Gaps 8;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOQNVFSCSVMHAEALHNNHYTKQSLSPGK 240
DB 279 PVLDSVGSFFLYSKLTVDKSRWQOQNVFSCSVMHAEALHNNHYTKQSLSPGK 330
QY 241 GGGSGGGGFTPTVKILQSSCDGGGHPPTTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300
DB 331 ----- 330
QY 301 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQGHTFEDSTKKC-ADSNPRGVS 359
DB 331 -----DKTHTC-----PPCPAPELLGGPS 349
QY 360 AYLRSRSPD-LFIRKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSTRKEEKORNGT 418
DB 350 VFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNST 409
QY 419 LTVSTLPTVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGS 478
DB 410 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL-----PPS 464
QY 479 RDKRT-----LACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLV 533
DB 465 RDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTTPVVLDSGSGFFLYSKLTV 522
QY 534 TRAEWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 569
DB 523 DKSRWQOQNVFSCSVMHAEALHNNHYT-QKSLSPGK 557

RESULT 7
US-11-022-289-2
; Sequence 2, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185931/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-5

Query Match          49.4%; Score 1511; DB 7; Length 557;
Best Local Similarity 53.1%; Pred. No. 1.5e-67;
Matches 306; Conservative 48; Mismatches 98; Indels 124; Gaps 8;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOQNVFSCSVMHAEALHNNHYTKQSLSPGK 240
DB 279 PVLDSVGSFFLYSKLTVDKSRWQOQNVFSCSVMHAEALHNNHYTKQSLSPGK 330
QY 241 GGGSGGGGFTPTVKILQSSCDGGGHPPTTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300
DB 331 ----- 330
QY 301 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQGHTFEDSTKKC-ADSNPRGVS 359
DB 331 -----DKTHTC-----SPCPAPELLGGPS 349
QY 360 AYLRSRSPD-LFIRKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSTRKEEKORNGT 418
DB 350 VFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNST 409
QY 419 LTVSTLPTVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGS 478
DB 410 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL-----PPS 464
QY 479 RDKRT-----LACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLV 533
DB 465 RDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTTPVVLDSGSGFFLYSKLTV 522
QY 534 TRAEWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 569
DB 523 DKSRWQOQNVFSCSVMHAEALHNNHYT-QKSLSPGK 557

RESULT 7
US-11-022-289-2
; Sequence 2, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185931/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-5

Query Match          49.3%; Score 1510; DB 7; Length 557;
Best Local Similarity 52.8%; Pred. No. 1.7e-67;
Matches 304; Conservative 50; Mismatches 98; Indels 124; Gaps 8;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOQNVFSCSVMHAEALHNNHYTKQSLSPGK 240
DB 279 PVLDSVGSFFLYSKLTVDKSRWQOQNVFSCSVMHAEALHNNHYTKQSLSPGK 330
QY 241 GGGSGGGGFTPTVKILQSSCDGGGHPPTTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300
DB 331 ----- 330
QY 301 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQGHTFEDSTKKC-ADSNPRGVS 359
DB 331 -----DKTHTC-----PPCPAPELLGGPS 349
QY 360 AYLRSRSPD-LFIRKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSTRKEEKORNGT 418
DB 350 VFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNST 409
QY 419 LTVSTLPTVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGS 478
DB 410 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL-----PPS 464
QY 479 RDKRT-----LACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLV 533
DB 465 REEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTTPVVLDSGSGFFLYSKLTV 522
QY 534 TRAEWEQKDEFICRAVHEAASPSQTVQRAVSNVPGK 569
DB 523 DKSRWQOQNVFSCSVMHAEALHNNHYT-QKSLSPGK 557

RESULT 8
US-11-022-289-3
; Sequence 3, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185931/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; 
```


US-11-022-289-3		Query Match		48.9%; Score 1497.5; DB 7; Length 548;	
		Best Local Similarity		52.3%; Pred. No. 6.7e-67;	
		Matches 301; Conservative		49; Mismatches 94; Indels 131; Gaps 7;	
Qy	1	EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60		
Db	99	EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	158		
Qy	61	NWYVDGVEHNHVKTPREEQYNSTYRVSVLTCLVKGFPSPDIQVWNGKCKVSNKALPAPIEKT	120		
Db	159	NWYVDGVEHNHVKTPREEQYNSTYRVSVLTCLVKGFPSPDIQVWNGKCKVSNKALPAPIEKT	218		
Qy	121	ISAKVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIQVWNGKCKVSNKALPAPIEKT	180		
Db	219	ISAKVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIQVWNGKCKVSNKALPAPIEKT	278		
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYQORSLSLSPKVEGGGSG	240		
Db	279	PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNHYQORSLSLSPKVEGGGSG	334		
Qy	241	GGSGGGGSPPTPVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVD	300		
Db	335	-----TPPT-----PSPSTPTPTSPSC-----	351		
Qy	301	LSTASTTQEGELASTQSELTLQKHWLSDRTYTCQVTYOQHTFEDSTKCADSNPRGVA	360		
Db	352	-----CHPR-----	356		
Qy	361	YLSRPSFDFIRKSPITITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKORNGTL	420		
Db	357	SLHRPALEDLLGSEANLTCTLTGLRDASG-VITFTWTFPSGKSAVQG--PPERDLGCGYS	413		
Qy	421	VTSTLPGVTRDMEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSR	479		
Db	414	VSSVLPGCAEPWNGHKTFTCTAAYPE-SKTPLTATLSKSGNTFRPEVHLLPPSEELALN	472		
Qy	480	DKETLACLIQNFPEDISVQWLHNEVQLPDARHSTTQPKTKGSG---FFVFSRLEVTRA	536		
Db	473	ELVTLTCLARGFPKQVLRWLGQSQELPREKTLTWASRQSPQSGITTFATVSLRVAE	532		
Qy	537	EWQKDEFFICRAVHEAASPSQTVQRAVSNPGK	569		
Db	533	DWKKGDTFSCWVGHEAL-PLAFTQKTIDRLAGK	564		
RESULT 10					
US-11-022-289-11					
; Sequence 11, Application US/11022289					
; Publication No. US20050249723A1					
; GENERAL INFORMATION:					
; APPLICANT: Lazar, Gregory Alan					
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES					
; FILE REFERENCE: 185831/US/2					
; CURRENT APPLICATION NUMBER: US/11/022,289					
; CURRENT FILING DATE: 2004-12-21					
; PRIOR FILING DATE: 2004-12-21					
; PRIOR FILING DATE: 2003-12-22					
; NUMBER OF SEQ ID NOS: 15					
; SOFTWARE: PatentIn version 3.3					
; SEQ ID NO 11					
; LENGTH: 330					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-11-022-289-11					
Query Match		40.0%; Score 1225; DB 7; Length 330;			
Best Local Similarity		97.0%; Pred. No. 6.5e-54;			
Matches 225; Conservative		3; Mismatches 4; Indels 0; Gaps 0;			
Qy	1	EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60		
Db	99	EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	158		
Qy	61	NWYVDGVEHNHVKTPREEQYNSTYRVSVLTCLVKGFPSPDIQVWNGKCKVSNKALPAPIEKT	120		
Db	159	NWYVDGVEHNHVKTPREEQYNSTYRVSVLTCLVKGFPSPDIQVWNGKCKVSNKALPAPIEKT	218		
US-11-022-289-10					
Query Match		46.2%; Score 1412.5; DB 7; Length 564;			
Best Local Similarity		52.0%; Pred. No. 8.7e-63;			
Matches 298; Conservative		37; Mismatches 127; Indels 111; Gaps 10;			

Qy	121	ISKAKVQPREPVYITLPSRDELTKQVSLTCLVKGYPSDIAVWESNQCPENNYKTTTP	180
Db	219	ISKAKVQPREPVYITLPSRDELTKQVSLTCLVKGYPSDIAVWESNQCPENNYKTTTP	278
Qy	181	PVLDSVGSFPLYKSLTVDKSRWQGNVFCSMWEALHNYHQFSLSLSPGK	232
Db	279	PVLDSVGSFPLYKSLTVDKSRWQGNVFCSMWEALHNYHQFSLSLSPGK	330

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RESULT 11
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

```

RESULT 12
US-11-016-503-6
; Sequence 6, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852

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; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-503-6

Query Match      40.0%; Score 1235; DB 7; Length 452;
Best Local Similarity 97.0%; Pred. No. 8.4e-54;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1  EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db      221 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 280

Qy      61  NWTVDGVEVHNVTCKPREEQYNTYRVSVSLTVLHQNMNGKEYCKVKVSNKALPAPIEKT 120
Db      281 NWTVDGVEVHNVTCKPREEQYNTYRVSVSLTVLHQDNLNGKEYCKVKVSNKALPAPIEKT 340

Qy      121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSPSDIAVEVESNGQPENNYKTTTP 180
Db      341 ISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSPSDIAVEVESNGQPENNYKTTTP 400

Qy      181 PVLDSVGSFPFLYSKGLTVDKSRWQOQGNVFVCSVMHEALHNHYQQRSLSPK 232
Db      401 PVLDSGSPFLYSKGLTVDKSRWQOQGNVFVCSVMHEALHNHYTKQSLSPK 452

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RESULT 13
US-10-949-720-390
; Sequence 390, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kerteszy, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949, 720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454, 432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454, 300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC-FC protein
US-10-949-720-390

```

```
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 288 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 347
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 407
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 408 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 459
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RESULT 14
US-11-016-503-8
; Sequence 8, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016.503
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-8
```

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Query Match 40.0%; Score 1225; DB 7; Length 462;
Best Local Similarity 97.0%; Pred. No. 8.6e-54;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 231 EPKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 290
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 291 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 350
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 351 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 410
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 411 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 462
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RESULT 15
US-10-835-475-11
; Sequence 11, Application US/10835475
; Publication No. US20050244410A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: Toll-Like Receptor Binding Agents and Uses Thereof
; FILE REFERENCE: CEN5022 USNP
; CURRENT APPLICATION NUMBER: US/10/835,475
; CURRENT FILING DATE: 2004-04-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
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; LENGTH: 489
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Predicted Mature Form of TLR9 EC260-Fc Fusion
US-10-835-475-11

Query Match 40.0%; Score 1225; DB 1; Length 489;
Best Local Similarity 96.1%; Pred. No. 9e-54;
Matches 224; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 61
Db 238 PKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 297
Qy 62 WYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 121
Db 298 WYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 357
Qy 122 SKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 181
Db 358 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 417
Qy 182 VLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGKVE 234
Db 418 VLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGKID 470
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Search completed: November 30, 2005, 00:46:53
Job time : 13 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2005, 00:32:33 ; Search time 168 Seconds

(without alignments)
1415.148 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHTCPCPAPPELL.....HEAASPSQTVQRAVSNVNGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3060	100.0	569	3	US-09-847-208-7
2	3060	100.0	569	4	US-10-000-439-7
3	1775	58.0	574	4	US-10-047-542-45
4	1775	58.0	574	4	US-10-214-524-37
5	1775	58.0	574	4	US-10-050-902-176
6	1775	58.0	574	4	US-10-050-898-176
7	1766	57.7	427	3	US-09-847-208-5
8	1766	57.7	427	4	US-10-000-439-5
9	1766	57.7	428	3	US-09-916-230-1
10	1766	57.7	428	3	US-09-949-375A-1
11	1766	57.7	428	4	US-10-047-542-60
12	1766	57.7	428	4	US-10-363-954A-1
13	1755	57.4	441	3	US-09-949-375A-7
14	1755	57.4	441	4	US-10-363-954A-7
15	1754.5	57.3	497	5	US-10-872-932A-35
16	1754.5	57.3	497	5	US-10-810-881A-34
17	1754.5	57.3	497	5	US-10-981-936-34
18	1733.5	56.7	586	5	US-10-627-556-384
19	1729	56.5	592	4	US-10-207-655-334
20	1729	56.5	592	5	US-10-627-556-129
21	1727	56.4	648	5	US-10-627-556-180
22	1725.5	56.4	648	5	US-10-627-556-184
23	1725	56.3	635	5	US-10-627-556-176
24	1721.5	56.3	593	3	US-10-627-556-248
25	1707	55.8	320	3	US-09-847-208-6
26	1707	55.8	320	4	US-10-000-439-6
27	1707	55.8	323	3	US-09-949-375A-2

ALIGNMENTS

RESULT 1

US-09-847-208-7

; Sequence 7, Application US/09847208

; Publication No. US20030082190A1

; GENERAL INFORMATION:

; APPLICANT: Saxon, Andrew

; APPLICANT: Zhang, Ke

; APPLICANT: Zhu, Daocheng

; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES

; FILE REFERENCE: UC67.002A

; CURRENT APPLICATION NUMBER: US/09/847,208

; CURRENT FILING DATE: 2001-05-01

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IGG1) to CH2-CH3-CH4

; OTHER INFORMATION: (IGF)

; US-09-847-208-7

Query Match 100.0%; Score 3060; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 5.5e-193;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EPKSCDKTHTCPCPAPPELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	Sequence 4, Appli
Db	1	EPKSCDKTHTCPCPAPPELLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	Sequence 6, Appli
QY	61	NWYVDGVEVHNKPKPEEQNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT	120	Sequence 2, Appli
Db	61	NWYVDGVEVHNKPKPEEQNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT	120	Sequence 4, Appli
QY	121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKPTP	180	Sequence 6, Appli
Db	121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKPTP	180	Sequence 2, Appli
QY	181	PVLDSVSGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHQQRSLSLSPGKVEGGSGG	240	Sequence 4, Appli
Db	181	PVLDSVSGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHQQRSLSLSPGKVEGGSGG	240	Sequence 6, Appli
QY	241	GGSGGGGSFPTPTVKILOSQCDGGHFPPTIQLCLVSGYTPGTINTWLTDGQVMDVD	300	Sequence 2, Appli
Db	241	GGSGGGGSFPTPTVKILOSQCDGGHFPPTIQLCLVSGYTPGTINTWLTDGQVMDVD	300	Sequence 4, Appli
QY	301	LSTASTTQEGELASTQSELTLSQKHWSLDRVTTCQVYQGHFTFEDSTKCADSNPRGVS	360	Sequence 10, Appli
				Sequence 13, Appli

Db 301 LSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVYQGHTEPDSSTKKCADSNPRGVS 360

Qy 361 YLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLT 420

Db 361 YLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLT 420

Qy 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480

Db 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480

Qy 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540

Db 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540

Qy 541 KDEFICRAVHEAASPSQTVQRAVSVNPGK 569

Db 541 KDEFICRAVHEAASPSQTVQRAVSVNPGK 569

RESULT 2

US-10-000-439-7

; Sequence 7, Application US/10000439

; Publication No. US20030064063A1

; GENERAL INFORMATION:

; APPLICANT: Saxon, Andrew

; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR

; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

; FILE REFERENCE: UC067.004A

; CURRENT APPLICATION NUMBER: US/10/000,439

; CURRENT FILING DATE: 2001-10-24

; PRIOR APPLICATION NUMBER: US 09/847,208

; PRIOR FILING DATE: 2001-05-01

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3

; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (Ige) sequence

US-10-000-439-7

Query Match 100.0%; Score 3060; DB 4; Length 569;

Best Local Similarity 100.0%; Pred. No. 5.5e-193;

Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Db 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNVTKPREQYNSTYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120

Db 61 NWYVDGVEVHNVTKPREQYNSTYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120

Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTP 180

Db 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTP 180

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNYQKRSLSLSPGKVEGGGSG 240

Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNYQKRSLSLSPGKVEGGGSG 240

Qy 241 GGGSGGGGSPPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300

Db 241 GGGSGGGGSPPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300

Qy 301 LSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVYQGHTEPDSSTKKCADSNPRGVS 360

Db 301 LSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVYQGHTEPDSSTKKCADSNPRGVS 360

Qy 361 YLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLT 420

Db 361 YLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLT 420

Qy 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480

Db 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480

Qy 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540

Db 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540

Qy 541 KDEFICRAVHEAASPSQTVQRAVSVNPGK 569

Db 541 KDEFICRAVHEAASPSQTVQRAVSVNPGK 569

RESULT 3

US-10-047-542-45

; Sequence 45, Application US/10047542

; Publication No. US20020168367A1

; GENERAL INFORMATION:

; APPLICANT: LARRICK, JAMES W.

; APPLICANT: WYCOFF, KEITH L.

; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

; TITLE OF INVENTION: AND BACTERIAL DISEASES

; FILE REFERENCE: 030905.0004.CIP1

; CURRENT APPLICATION NUMBER: US/10/047,542

; CURRENT FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: PCT/US01/13932

; PRIOR FILING DATE: 2001-04-28

; PRIOR APPLICATION NUMBER: 60/200,298

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 45

; LENGTH: 574

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-047-542-45

Query Match 58.0%; Score 1775; DB 4; Length 574;

Best Local Similarity 77.3%; Pred. No. 2e-108;

Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

Qy 120 TISKAKVQPREPOVYTLPPSRDELTKNOVSLT--CLVKGYFSPSDIAVEWESNGQPENNYK 177

Db 143 TVSSASTQ--SPSVFPLTRCCKNIPSNATSVLGLCLATGFPPEPVMTWDT--GSLNGTTM 199

Qy 178 TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNY-QQRSLSLSPGKVEG 235

Db 200 TLPATTTLSGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC----- 251

Qy 236 GGGSGGGGSGGSPPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQ 295

Db 252 -----SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQ 300

Qy 296 VMDVDLSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVYQGHTEPDSSTKKCADSNP 355

Db 301 VMDVDLSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVYQGHTEPDSSTKKCADSNP 360

Qy 356 RGVSAVLSRSPSPDLFIKSPPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQ 415

Db 361 RGVSAVLSRSPSPDLFIKSPPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQ 420

Qy 416 NGFLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEW 475

Db 421 NGFLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEW 480

Qy 476 PGSRDKRTKLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTR 535

Db 481 PGSRDKRTKLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTR 540

Qy 536 AEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK 569

186 VGSFPLYSKLTVDKSRWQGNVFCVSMHEALHNHY-QORSLSLSPGKVEGGGGGGGS 244
62 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDKTFVC----- 104
245 GGGGSFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 304
105 --SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 162
305 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 364
163 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 222
365 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQKNGTLTVTST 424
223 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQKNGTLTVTST 282
425 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
283 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 342
485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 544
343 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 402
545 ICRAVHEAASPSQTVQRAVSNVPGK 569
403 ICRAVHEAASPSQTVQRAVSNVPGK 427

RESULT 9

US-09-916-230-1
; Sequence 1, Application US/09916230
; Patent No. US2002014622A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; TITLE OF INVENTION: Compositions for Inducing Self-Specific Anti-IgE
; FILE REFERENCE: 1700.0140001
; CURRENT APPLICATION NUMBER: US/09/916,230
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,841
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-230-1

Query Match 57.7%; Score 1766; DB 3; Length 428;
Best Local Similarity 78.0%; Pred. No. 5.6e-108;
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;

129 REPQVTLPPSRDELTKNOVSLT-CLVKGFPVPSDIAVWESNGQPENNYKTP-PVLDS 185
4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTTMTLPATLTL 62
186 VGSFPLYSKLTVDKSRWQGNVFCVSMHEALHNHY-QORSLSLSPGKVEGGGGGGGS 244
63 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDKTFVC----- 105
245 GGGGSFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 304
106 --SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 163
305 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 364
164 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 223
365 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQKNGTLTVTST 424

Db 224 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQKNGTLTVTST 283
Qy 425 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
Db 284 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343
Qy 485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 544
Db 344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 403
Qy 545 ICRAVHEAASPSQTVQRAVSNVPGK 569
Db 404 ICRAVHEAASPSQTVQRAVSNVPGK 428

RESULT 10

US-09-949-375A-1
; Sequence 1, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 428
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (11)..(116)
; OTHER INFORMATION: Human IgE heavy chain C1 domain
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (209)..(216)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (205)..(219)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (315)..(323)
; OTHER INFORMATION: Epitope including C3C4 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (244)..(251)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (272)..(280)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (301)..(311)
; OTHER INFORMATION: Epitope in FG loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (317)..(320)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (321)..(422)
; OTHER INFORMATION: Human IgE heavy chain C4 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (217)..(316)
; OTHER INFORMATION: Human IgE heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN

QY	186	VGSFELYSLKLTVDKSRWQQGNVFCSCVMHEALHNHY-QQRSLSLSLSPGKVGCGGGGGGS	244
Db	63	SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC-----	105
QY	245	GGGSGFTPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	304
Db	106	--SRDFTPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	163
QY	305	STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSR	364
Db	164	STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSR	223
QY	365	PSPFDLFIKRSPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKORNGTLTVTST	424
Db	224	PSPFDLFIKRSPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKORNGTLTVTST	283
QY	425	LPVGTTRDWIEGETYQCRVTHPHPLRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL	484
Db	284	LPVGTTRDWIEGETYQCRVTHPHPLRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL	343
QY	485	ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEF	544
Db	344	ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEF	403
QY	545	ICRAVHEAASPQTVQRAVSVNPGK	569
Db	404	ICRAVHEAASPQTVQRAVSVNPGK	428
RESULT 12			
US-10-363-954A-1			
; Sequence 1, Application US/10363954A			
; Publication No. US20040156838A1			
; GENERAL INFORMATION:			
; APPLICANT: KLYSNER, Steen et al.			
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE			
; FILE REFERENCE: 4614-0115P			
; CURRENT APPLICATION NUMBER: US/10/363,954A			
; CURRENT FILING DATE: 2003-03-06			
; PRIOR APPLICATION NUMBER: US 60/232,831			
; PRIOR FILING DATE: 2000-09-15			
; PRIOR APPLICATION NUMBER: DK PA 2000 01326			
; PRIOR FILING DATE: 2000-09-06			
; NUMBER OF SEQ ID NOS: 38			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 1			
; LENGTH: 428			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: DOMAIN			
; LOCATION: (11)..(116)			
; OTHER INFORMATION: Human IgE heavy chain C1 domain			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (209)..(216)			
; OTHER INFORMATION: Linker between domains C2 and C3			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (205)..(219)			
; OTHER INFORMATION: Epitope including C2C3 linker			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (315)..(323)			
; OTHER INFORMATION: Epitope including C3C4 linker			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (244)..(251)			
; OTHER INFORMATION: Epitope in BC loop			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (272)..(280)			
; OTHER INFORMATION: Epitope in DE loop			

QY	129	REPQVYTLPPSRDELTKNOVSLT--CLVKGFPYSDIAVESNQPPENNYKTTTP-PVLDS	185
Db	4	QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMTWDT-GSLNGTTMTLPAATLTL	62
QY	186	VGSFELYSLKLTVDKSRWQQGNVFCSCVMHEALHNHY-QQRSLSLSLSPGKVGCGGGGGGS	244
Db	63	SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC-----	105
QY	245	GGGSGFTPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	304
Db	106	--SRDFTPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	163
QY	305	STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSR	364
Db	164	STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSR	223
QY	365	PSPFDLFIKRSPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKORNGTLTVTST	424
Db	224	PSPFDLFIKRSPTITCLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKORNGTLTVTST	283
QY	425	LPVGTTRDWIEGETYQCRVTHPHPLRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL	484
Db	284	LPVGTTRDWIEGETYQCRVTHPHPLRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL	343
QY	485	ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEF	544
Db	344	ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEF	403
QY	545	ICRAVHEAASPQTVQRAVSVNPGK	569
Db	404	ICRAVHEAASPQTVQRAVSVNPGK	428
RESULT 11			
US-10-047-542-60			
; Sequence 60, Application US/10047542			
; Publication No. US20020168367A1			
; GENERAL INFORMATION:			
; APPLICANT: LARRICK, JAMES W.			
; APPLICANT: WYCOFF, KEITH L.			
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL			
; TITLE OF INVENTION: AND BACTERIAL DISEASES			
; FILE REFERENCE: 030905.0004.C1P1			
; CURRENT APPLICATION NUMBER: US/10/047,542			
; PRIOR FILING DATE: 2001-10-26			
; PRIOR APPLICATION NUMBER: PCT/US01/13932			
; PRIOR FILING DATE: 2001-04-28			
; PRIOR APPLICATION NUMBER: 60/200,298			
; PRIOR FILING DATE: 2000-04-28			
; NUMBER OF SEQ ID NOS: 101			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 60			
; LENGTH: 428			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-047-542-60			
Query Match			
Best Local Similarity 57.7%; Score 1766; DB 4; Length 428;			
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;			
QY	129	REPQVYTLPPSRDELTKNOVSLT--CLVKGFPYSDIAVESNQPPENNYKTTTP-PVLDS	185
Db	4	QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMTWDT-GSLNGTTMTLPAATLTL	62

Db 224 PSFDFLRKSPITCLVVDLAKSGIVNLTWSRAGKPVNHSRKEEKQKNGTLTVTST 283
Qy 425 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
Db 284 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343
Qy 485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 544
Db 344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 403
Qy 545 ICRAVHEAASPQTQVQRAVSNP 567
Db 404 ICRAVHEAASPQTQVQRAVSNP 426

RESULT 14
US-10-363-954A-7
; Sequence 7, Application US/10363954A
; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (11)..(106)
; OTHER INFORMATION: Ige heavy chain C1 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (113)..(208)
; OTHER INFORMATION: Ige heavy chain C2 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (217)..(317)
; OTHER INFORMATION: Ige heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (321)..(422)
; OTHER INFORMATION: Ige heavy chain C4 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (427)..(441)
; OTHER INFORMATION: MIGIS fragment
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (209)..(216)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (318)..(320)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (205)..(219)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (315)..(323)
; OTHER INFORMATION: Epitope including C3C4 linker
; FEATURE:

; NAME/KEY: MISC FEATURE
; LOCATION: (244)..(251)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (272)..(280)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (301)..(311)
; OTHER INFORMATION: Epitope in FG loop
US-10-363-954A-7
Query Match 57.4%; Score 1755; DB 4; Length 441;
Best Local Similarity 77.9%; Pred. No. 3.le-107;
Matches 345; Conservative 17; Mismatches 57; Indels 24; Gaps 7;
Qy 129 REPOVYTLPPSRDELTKNOVSLT--CLVKGFPVPSDIAVWESNGQPENNYKTP-PVLDS 185
Db 4 QSPSPFPLTRCCKNIPSNATSVTLGCLATGYFPFVPMVTWDT-GSLNGTTMTLPATTLTL 62
Qy 186 VGSFFLYSKLTVDKSRWQGNVFSVMEALHNYH-QQRSLSLSPKVEGGGGGGGS 244
Db 63 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDNKTFSVC----- 105
Qy 245 GGGGSPPTPVKILQSSCDGGGHPPTIQLLCLVSGYTGTTINITWLEQVMDVDLSTA 304
Db 106 --SRDFTPTPVKILQSSCDGGGHPPTIQLLCLVSGYTGTTINITWLEQVMDVDLSTA 163
Qy 305 STTQEGELASTOSELTLKOKHLSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSR 364
Db 164 STTQEGELASTOSELTLKOKHLSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSR 223
Qy 365 PSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNGTLTVTST 424
Db 224 PSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKQKNGTLTVTST 283
Qy 425 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
Db 284 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343
Qy 485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 544
Db 344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 403
Qy 545 ICRAVHEAASPQTQVQRAVSNP 567
Db 404 ICRAVHEAASPQTQVQRAVSNP 426

RESULT 15
US-10-872-932A-35
; Sequence 35, Application US/10872932A
; Publication No. US20050033029A1
; GENERAL INFORMATION:
; APPLICANT: Jin lu
; TITLE OF INVENTION: ENGINEERED ANTI-TARGET IMMUNOGLOBULIN DERIVED PROTEINS
; FILE REFERENCE: CEN5031NP
; CURRENT APPLICATION NUMBER: US/10/872,932A
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/483,654
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-932A-35
Query Match 57.3%; Score 1754.5; DB 5; Length 497;
Best Local Similarity 77.5%; Pred. No. 3.8e-107;
Matches 347; Conservative 17; Mismatches 57; Indels 27; Gaps 8;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 29, 2005, 23:38:37 ; Search time 189 Seconds

(without alignments)
1322.786 Million cell updates/sec

Title: US-09-847-208b-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHTCPCPAPELL.....HEAAPSQTQRAVSNVPGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3060	100.0	569	AAO19668	Aao19668 GE2 fusio
2	1775	58.0	574	ABG94250	Abg94250 Human Ige
3	1775	58.0	574	ABG80562	Abg80562 Human Ige
4	1775	58.0	574	ABP96592	Abp96592 Human Ige
5	1775	58.0	574	ADP97368	Adp97368 Human imm
6	1766	57.7	427	AAO19666	Aao19666 Human Ige
7	1766	57.7	428	AAW47863	Aaw47863 Human Ige
8	1766	57.7	428	AAU80283	Aau80283 Human Ige
9	1766	57.7	428	AAW50940	Aaw50940 Human imm
10	1766	57.7	428	AAE35113	Aae35113 Human imm
11	1766	57.7	428	ADD48440	Add48440 Human Pro
12	1766	57.7	428	ADP97382	Adp97382 Human Ige
13	1760	57.5	493	AAW40065	Aaw40065 Sequence
14	1755	57.4	441	AAU80287	Aau80287 Human Ige
15	1754.5	57.3	497	ADW24784	Adw24784 Human var
16	1754.5	57.3	497	ADW24742	Adw24742 Human var
17	1754.5	57.3	497	ADZ08809	Adz08809 Mammalian
18	1754.5	57.3	497	ADZ08940	Adz08940 Mammalian
19	1754.5	57.3	497	ADZ44466	Adz44466 Human imm
20	1754.5	57.3	497	AEA16541	Aea16541 Human MCP
21	1754.5	57.3	497	AEB72776	Aeb72776 Anti-Ltal
22	1733.5	56.7	586	ADY22009	Ady22009 Antibody
23	1729	56.5	592	ADD25773	Add25773 Binding d
24	1729	56.5	592	ADY21754	Ady21754 Antibody

25	1727	56.4	648	9	ADY21805	Ady21805 Antibody
26	1725.5	56.4	648	9	ADY21809	Ady21809 Antibody
27	1725	56.4	635	9	ADY21801	Ady21801 Antibody
28	1723	56.3	428	2	AAR42950	Aar42950 Human IGE
29	1721.5	56.3	593	9	ADY21873	Ady21873 Antibody
30	1720.5	56.2	425	6	AAE35114	Aae35114 Human imm
31	1707	55.8	320	6	AAO19667	Aao19667 Human IGE
32	1707	55.8	323	5	AAU80286	Aau80286 Human IGE
33	1707	55.8	323	5	AAU80285	Aau80285 Human IGE
34	1707	55.8	323	5	AAU80284	Aau80284 Human IGE
35	1707	55.8	324	2	AAR83559	Aar83559 Fc(eps)ilo
36	1707	55.8	325	2	AAR75225	Aar75225 Human IGE
37	1707	55.8	325	2	AAR77241	Aar77241 Human IGE
38	1707	55.8	327	9	ADY21849	Ady21849 Human IGE
39	1707	55.8	331	3	AAO3642	Aao3642 Human IGE
40	1707	55.8	331	7	ADD25768	Add25768 Binding d
41	1707	55.8	331	9	ADY21799	Ady21799 Human IGE
42	1707	55.8	331	9	ADY21722	Ady21722 Human IGE
43	1707	55.8	367	1	AAP80291	Aap80291 Interleuk
44	1705.5	55.7	426	6	ABP96581	Abp96581 Chimpanze
45	1701	55.6	325	3	AAV79994	Aay79994 Human imm

ALIGNMENTS

RESULT 1

AAO19668

ID AAO19668 standard; protein; 569 AA.

XX AC AAO19668;

XX AC AAO19668;

DT 28-MAR-2003 (first entry)

XX GE2 fusion protein for use in treating immune diseases.

XX Human; IGE; immunoglobulin E; immunotherapy; immune disease;

XX Fcepsilon receptor; autoimmune disease; constant region; heavy chain;

XX antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2;

XX antiarthritic; antirheumatic; antidiabetic; neuroprotective;

XX fusion protein.

XX Synthetic.

OS Unidentified.

XX WO200288317-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013527.

XX 01-MAY-2001; 2001US-00847208.

XX 24-OCT-2001; 2001US-00000439.

XX (REGC) UNIV CALIFORNIA.

XX Saxon A, Zhang K, Zhu D;

XX WPI; 2003-103456/09.

DR New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IGE receptor, usefull for treating IGE-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX Claim 35; Fig 7; 116pp; English.
XX The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IGE
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IGE receptor

CC	(FcepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IGE-mediated biological response, preferably an IGE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-1 diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is a gammahinge-CHgamma2-CHgamma3-(Gly4Ser)3-CHepsilon2-CHepsilon3-CHepsilon3 fusion protein (designated GB2) of the invention	OS	Homo sapiens.
CC		OS	Synthetic.
CC		PN	WO200256905-A2.
CC		XX	25-JUL-2002.
CC		XX	21-JAN-2002; 2002WO-IB000166.
CC		XX	19-JAN-2001; 2001US-0262379P.
CC		PR	04-MAY-2001; 2001US-0288549P.
CC		PR	05-OCT-2001; 2001US-0326998P.
CC		PR	07-NOV-2001; 2001US-0331045P.
CC		XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.
PA		XX	Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P; Piossek C;
PI		XX	WPI; 2002-627351/67.
PI		XX	Molecular antigen array used in the production of vaccines for infectious diseases.
DR		XX	Disclosure; Page 389-390; 441pp; English.
PT		XX	This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffold comprising a core particle selected from a core particle of a non-natural origin and a core particle of natural origin and an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (Abetal-42) or its fragment and where the second attachment site is selected from an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Qbeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention
XX		XX	Sequence 574 AA;
XX		XX	Query Match 58.0%; Score 1775; DB 5; Length 574;
XX		XX	Best Local Similarity 77.3%; Pred. No. 5.6e-114; Indels 26; Gaps 8;
XX		XX	Matches 351; Conservative 17; Mismatches 60;
QY	120	TIISKAKVQPREPQVYTLPPSRDELTKNQVSLT--CLVKGFPSPDIAVWESNGQPENNYK	177
DB	143	TVSSASTQ--SPSVPLTFCKNIPSNATSVTLGCLATGYFPEPVNVTWDT--GSLNGTMM	199
QY	178	TTP-PVLDSVGFYLYSKLTVDKSRWQGNVFCSCVMHEALHNHY--QQRSLSPGKVEG	235
DB	200	TLPATTLTSLGSHYATISLLTV--SGAWAK-QMPTCRVAHTPSSTWDVNDKTFVC-----	251
QY	236	GGSGGGGGGGSGSTPPTVKILOSGCDGGHFPPTIQLCLVSGYTPGTINTWLEDGQ	295
DB	252	-----SRDFTPTPTVKILOSCDGGHFPPTIQLCLVSGYTPGTINTWLEDGQ	300
QY	296	VMDVLDLSTASTTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKCADSNP	355
DB	301	VMDVLDLSTASTTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKCADSNP	360

QY 356 RGVSAVLSRSPFDLFIKSPPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKOR 415
Db |||||
QY 361 RGVSAVLSRSPFDLFIKSPPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKOR 420
Db |||||
QY 416 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 475
Db |||||
QY 421 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 480
Db |||||
QY 476 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 535
Db |||||
QY 481 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 540
Db |||||
QY 536 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 569
Db |||||
QY 541 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 574
Db |||||

RESULT 3

ABG80562

ID ABG80562 standard; protein; 574 AA.

AC

XX ABG80562;

DT 29-NOV-2002 (first entry)

XX

DE Human IgE heavy chain.

XX

KW Molecular antigen array; vaccine; antigen; antimicrobial;

KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;

KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;

KW adult respiratory distress syndrome; ARDS; Crohn's disease;

KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;

KW Grave's disease; systemic lupus erythematosus; osteoporosis;

KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;

KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;

KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;

KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;

KW enterokinase; cysteine-containing linker.

XX

OS Homo sapiens.

XX

PN WO200256907-A2.

XX

XX 25-JUL-2002.

XX

XX 21-JAN-2002; 2002WO-IB000168.

XX

PR 19-JAN-2001; 2001US-0262379P.

PR

PR 04-MAY-2001; 2001US-0288549P.

PR

PR 05-OCT-2001; 2001US-0326998P.

PR

PR 07-NOV-2001; 2001US-0331045P.

XX

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVS) NOVARTIS PHARMA AG.

PA (MAUR/) MAURER P.

PA (LECH/) LECHNER F.

PA (ORTM/) ORTMANN R.

PA (LUEO/) LUEOEND R.

PA (STAU/) STAUFENBIEL M.

PA (FREY/) FREY P.

XX

XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;

PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;

XX

XX WPI; 2002-636514/68.

XX

XX Molecular antigen array used in the production of vaccines for infectious

PT diseases.

XX

XX Disclosure; Page 366-368; 418pp; English.

XX

XX The invention relates to a composition comprising: (a) a non-natural

CC molecular scaffold comprising: (i) a core particle selected from: (1) a

CC core particle of a non-natural origin; and (2) a core particle of natural
CC origin; and (ii) an organiser comprising at least one first attachment
CC site, where the organiser is connected to the core particle by at least
CC one covalent bond; (b) an antigen or antigenic determinant with at least
CC one second attachment site, where the antigen or antigenic determinant is
CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
CC attachment site is selected from: (i) an attachment site not naturally
CC occurring with the antigen or antigenic determinant; and (ii) an
CC attachment site naturally occurring with the antigen or antigenic
CC determinant, where the second attachment site is capable of association
CC through at least one non-peptide bond to the first attachment site; and
CC where the antigen or antigenic determinant and the scaffold interact
CC through the association to form an ordered and repetitive antigen array.
CC Also included is a process for producing a non-naturally occurring
CC ordered and repetitive antigen array. The composition is used in
CC immunisation and as a vaccine for diseases such as influenza, graft
CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
CC gravis, immunoproliferative disease lymphadenopathy,
CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
CC osteoporosis and infectious diseases. The present sequence is an antigen
CC for use in the array of the invention. The antigen is modified to possess
CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-
CC or C-terminal linker peptide which serves as the attachment point to a
CC virus like particle or bacterial protein (the scaffold protein)
XX

Sequence 574 AA;

Query Match 58.0%; Score 1775; DB 5; Length 574;
Best Local Similarity 77.3%; Pred. No. 5.6e-114;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;
QY 120 TISKAKVQPREPQVYTLPPSRDELTQKQVSLT--CLVKGFPVSDIAVWENSGQENNVK 177
Db |||||
QY 143 TVSSASTQ--SPSVFPLTRCCNKIPSNATSVTLGLCLATGYPPEPVMVTDWDT-GSLNGTTM 199
Db |||||
QY 178 TTP-PVLDSVGSFFLYSKLTVDKSRWQGVNFCVSMHEALHNYH-QQRSLSLSPGKVEG 235
Db |||||
QY 200 TLPATTLTLTGHYATISLLTV-SGAWAK-QMPTCRVAHTPSTWDVNDKTSVC----- 251
QY 236 GGGGGGGGGGGGFTPTVKILOSSCDGGGHFPPTIQLCLVSGYTPGTINITWLEDQ 295
Db |||||
QY 252 -----SRDFTPTVKILOSSCDGGGHFPPTIQLCLVSGYTPGTINITWLEDQ 300
QY 296 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVYQHTFEDSTKCADSNP 355
Db |||||
QY 301 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVYQHTFEDSTKCADSNP 360
QY 356 RGVSAVLSRSPFDLFIKSPPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKOR 415
Db |||||
QY 416 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 475
Db |||||
QY 421 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 480
QY 476 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 535
Db |||||
QY 481 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 540
Db |||||
QY 536 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 569
Db |||||
QY 541 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 574
Db |||||

RESULT 4

ABP96592

ID ABP96592 standard; protein; 574 AA.

XX

AC ABP96592;

QY 245 GGGGFTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 304
DB 106 --SRDFTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 163
QY 305 STTQEGELASTQSELTLISQKHLSDRITYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSR 364
DB 164 STTQEGELASTQSELTLISQKHLSDRITYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSR 223
QY 365 PSPFDLPFIRKSPITITCLVVDLAPSGKTVNLTWSRAGKPVNHSRKEEKORNGTLTWTST 424
DB 224 PSPFDLPFIRKSPITITCLVVDLAPSGKTVNLTWSRAGKPVNHSRKEEKORNGTLTWTST 283
QY 425 LPVGTREDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEYVAFATPEWPGSRDKRTL 484
DB 284 LPVGTREDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEYVAFATPEWPGSRDKRTL 343
QY 485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVTRAWEQKDEF 544
DB 344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVTRAWEQKDEF 403
QY 545 ICRVHAEAAASPSQTVQRAVSNPGK 569
DB 404 ICRVHAEAAASPSQTVQRAVSNPGK 428
RESULT 10
AAE35113
ID AAE35113 standard; protein; 428 AA.
AC AAE35113;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human immunoglobulin E (IgE) constant region.
XX
KW Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;
KW lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;
KW psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;
KW inflammatory bowel disease; insulin dependent diabetes; cell therapy;
KW Crohn's disease; allergic rhinitis; graft versus host disease; asthma;
KW transplant rejection; human; immunoglobulin E; IgE.
XX
OS Homo sapiens.
XX
PN WO200292773-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-US015341.
XX
PR 15-MAY-2001; 2001US-0291300P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Degraw J;
XX
XX WPI; 2003-120673/11.
DR
XX
XX Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases,
PT comprises culturing CD8+ T cells with antigen presenting cells to
PT activate precursor CD8+ T cells specific for T the cell epitopes.
XX
PS Disclosure; Fig 7; 49pp; English.
XX
XX The invention relates to a method of producing cytotoxic T lymphocytes
CC (CTLs) specific for one or more non-tumour self antigen T cell epitopes.
CC The method involves loading antigen presenting cells (APCs) having class
CC I major histocompatibility complex molecules with the T cell epitopes, T
CC and culturing the CD8+ T cells with the APCs to activate precursor CD8+ T
CC cells specific for the T cell epitopes. The invention is useful for
CC treating autoimmune disease including rheumatoid arthritis, psoriasis,
CC lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,
CC insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,

CC graft versus host disease and transplant rejection and/or allergic
CC disease such as food allergy, hay fever, allergic rhinitis, allergic
CC asthma and venom allergy. The invention is also useful in cell therapy.
CC The present sequence is human immunoglobulin E (IgE) constant region.
CC This protein is used in the exemplification of the invention. Note: This
CC sequence is stated to be the same as that shown in figure 10 (AAE35114)
CC of the specification. However these sequences differ
XX
SQ Sequence 428 AA;
Query Match 57.7%; Score 1766; DB 6; Length 428;
Best Local Similarity 78.0%; Pred. No. 1.6e-113;
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;
QY 129 RRPQVTLPPSRDELTKNOVSILT--CLVKGFTPSDIAVEWESNGQPNYKTP-PVLDS 185
DB 4 QSPSPVPLPRCKCKNTPSNATSVTLGLATGYFPPEVMVTWDT-GSLNGTTMTLPATTLTL 62
QY 186 VGSFFLYSKLTVDKSRWQGNVFCSSVMHEALHNY-QORSLSLSPGKVEGGGGGGGS 244
DB 63 SGHIATISLLTV-SGAWAK-QMFTCRVAHTPSTWDVNDKTSVC----- 105
QY 245 GGGGFTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 304
DB 106 --SRDFTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 163
QY 305 STTQEGELASTQSELTLISQKHLSDRITYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSR 364
DB 164 STTQEGELASTQSELTLISQKHLSDRITYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSR 223
QY 365 PSPFDLPFIRKSPITITCLVVDLAPSGKTVNLTWSRAGKPVNHSRKEEKORNGTLTWTST 424
DB 224 PSPFDLPFIRKSPITITCLVVDLAPSGKTVNLTWSRAGKPVNHSRKEEKORNGTLTWTST 283
QY 425 LPVGTREDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEYVAFATPEWPGSRDKRTL 484
DB 284 LPVGTREDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEYVAFATPEWPGSRDKRTL 343
QY 485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVTRAWEQKDEF 544
DB 344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVTRAWEQKDEF 403
QY 545 ICRVHAEAAASPSQTVQRAVSNPGK 569
DB 404 ICRVHAEAAASPSQTVQRAVSNPGK 428
RESULT 11
ADD48440
ID ADD48440 standard; protein; 428 AA.
XX
AC ADD48440;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAB59424, SEQ ID NO 14141.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
XX WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.


```
Db      63 SGHYATISLTV-SGAWAK-QMTICRVAHTPSSTDWVDNKTFSVC----- 105
QY      245 GGGGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 304
Db      106 --SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 163
QY      305 STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVAYLSR 364
Db      164 STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVAYLSR 223
QY      365 PSPFDLPIRKSPITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORNGTLTWST 424
Db      224 PSPFDLPIRKSPITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORNGTLTWST 283
QY      425 LPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
Db      284 LPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343
QY      485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVPSRLLEVTRAWEQKDEF 544
Db      344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVPSRLLEVTRAWEQKDEF 403
QY      545 ICRAVHEAASPSTQVQRAVSNPGK 569
Db      404 ICRAVHEAASPSTQVQRAVSNPGK 428

RESULT 14
AAP40065
ID AAP40065 standard; protein; 493 AA.
XX AAP40065;
XX
XX 25-MAR-2003 (revised)
XX 12-FEB-1992 (first entry)
XX
XX Sequence of human immunoglobulin E H-chain.
XX Antibody; allergy suppressor; immunological.
XX Homo sapiens.
XX EP102634-A.
XX
XX 14-MAR-1984.
XX
XX 03-SEP-1983; 83EP-00108699.
XX
XX 07-SEP-1982; 82JP-00156285.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kikuchi M, Kurokawa T, Onda H;
XX WPI; 1984-070437/12.
XX N-PSDB; AAN40062.
XX
XX Polypeptide having activity of human immunoglobulin E - prep'd. from host
XX transformed with recombinant DNA.
XX
XX Disclosure; Fig 2; 61pp; English.
XX
XX DNA encoding IgE H-chain and frags. is claimed (AAN40062). Transformant
XX contg. the DNA is also new, esp. Escherichia coli IFO- 14284, -5 and -6.
XX The transformant may be grown to produce a polypeptide of immunological
XX or biological activity equivalent to that of the human IgE H chain.
XX AAN40062 or frags. is pref. linked at a site downstream from a promoter,
XX e.g. rec A promoter (see AAN40064). (Updated on 25-MAR-2003 to correct PA
XX field.)
XX Sequence 493 AA;
```

```
Query Match      57.5%; Score 1760; DB 1; Length 493;
Best Local Similarity 77.0%; Pred. No. 5e-113;
Matches 349; Conservative 14; Mismatches 66; Indels 24; Gaps 7;

QY      120 TISKAKVQPREPOVYTLPPSRDELTKNQVSLT--CLVKGFPSPSDIAVESNGQPENNYK 177
Db      62 TVSSASTQ--SPSVFPLTRCKNIPSNATSVTLGCLATGYFPEPVMVWTDT-GSLNGTTM 118
QY      178 TTP-PVLDSVGGFFLYSLKLTVDKSRWQQGNVFSQSVMEALHNHYQORSLSLSPGKVEGG 236
Db      119 TLPATTLTLSGHYATISLTV-SGAWAK-QIETCRVAHTPSSTDWVDNKT----- 167
QY      237 GSGGGGGGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQV 296
Db      168 -----SVCSRDFPTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQV 220
QY      297 MDVDLSTASTTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPR 356
Db      221 MDVDLSTASTTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPR 280
QY      357 GVSAYLSRSPFDLPIRKSPITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORN 416
Db      281 GVSAYLSRSPFDLPIRKSPITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORN 340
QY      417 GTLTVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 476
Db      341 GTLTVTSTLPVGTDRWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 400
QY      477 GSRDKRTLACLQNFMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVPSRLLEVTRA 536
Db      401 GSRDKRTLACLQNFMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVPSRLLEVTRA 460
QY      537 EWEQKDEFICRAVHEAASPSTQVQRAVSNPGK 569
Db      461 EWEQKDEFICRAVHEAASPSTQVQRAVSNPGK 493

RESULT 14
AAU80287
ID AAU80287 standard; protein; 441 AA.
XX AAU80287;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human IgG heavy chain C1-C2-C3-C4 domains with MIGIS fragment.
XX IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
XX antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
XX heavy chain C domain; MIGIS.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX PH Domain 11..106
XX FT Domain /notes="IgE heavy chain C1 domain"
XX FT Domain 113..208
XX FT Region /label="IgE heavy chain C2 domain"
XX FT Region 205..219
XX FT Region /notes="Epitope including C2C3 linker"
XX FT Region 209..216
XX FT Domain /notes="Linker domain between C2 and C3 region"
XX FT Domain 217..317
XX FT Region /notes="IgE heavy chain C3 domain"
XX FT Region 244..251
XX FT Region /notes="Epitope in BC loop"
XX FT Region 244..251
XX FT Region /notes="Epitope in BC loop"
XX FT Region 272..280
XX FT Region /notes="Epitope in DE loop"
XX FT Region 301..311
```


FT	Region	/note= "Epitope in FG loop"	Db	284	LPVGRDWEGETYQCRVTHPLRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTL	343
FT	Region	315..323	Qy	485	ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLLEVTRAWEQKDEF	544
FT	Region	/note= "Epitope including C3C4 linker"	Db	344	ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLLEVTRAWEQKDEF	403
FT	Domain	318..320				
FT	Domain	/note= "Linker between domains C3 and C4"				
FT	Domain	321..422				
FT	Domain	/note= "Ige heavy chain C4 domain"				
FT	Domain	427..421				
FT	Domain	/note= "MIGIS fragment"				
XX	WO200220038-A2.					
XX	14-MAR-2002.					
XX	06-SEP-2001; 2001WO-DK000579.					
XX	06-SEP-2000; 2000DK-00001326.					
PR	15-SEP-2000; 2000US-0232831P.					
XX	(PHAR-) PHARMEXA AS.					
XX	Klyesner S, Von Hoegen P, Voldborg B, Gautam A;					
XX	WPI; 2002-383033/41.					
XX	Inducing immune response against autologous immunoglobulin E in an					
FT	animal, by effecting simultaneous presentation of cytotoxic T lymphocyte					
FT	epitope an/or B-cell epitope derived from the immunoglobulin.					
XX	Example; Page 116-117; 151pp; English.					
XX	This invention relates to a novel method for inducing an immune response					
CC	against autologous immunoglobulin E (IGE) in an animal. The method					
CC	comprises effecting simultaneous presentation of cytotoxic T lymphocyte					
CC	(CTL) epitope and/or B-cell epitope derived from Ige, and T helper cell					
CC	epitope (TH epitope) which is foreign to the animal, by antigen					
CC	presenting cells (APCs) of the animal's immune system. The epitopes of					
CC	the invention may be used as a vaccine against allergic diseases. The					
CC	method of the invention is useful for inducing an immune response against					
CC	autologous IGE in an animal, which is useful for downregulating					
CC	autologous IGE in the animal. This method is useful in the prevention and					
CC	treatment of allergic diseases such as anaphylaxis, allergic rhinitis,					
CC	asthma and atopic dermatitis. The present sequence represents the human					
CC	IGE heavy chain C1-C2-C3-C4 domains fused to the MIGIS fragment used to					
CC	create the epitopes of the invention					
XX	Sequence 441 AA;					
SQ	Query Match 57.4%; Score 1755; DB 5; Length 441;					
	Beat Local Similarity 77.9%; Pred. No. 9.7e-113;					
	Matches 345; Conservative 17; Mismatches 57; Indels 24; Gaps 7;					
Qy	129 REPQVYTLPPSRDELTKNOVSLT--CLVKGFPVPSDIAVEWESNGQPPENNYKTPP-PVLDS 185					
Db	4 QSPVFPLTRCKNIPSPNATSVTLGLATGYPPEPVMWTWDI-GSLNGTTWTLPATITL 62					
Qy	186 VGSFPLYSLKLTVDKRWQGNVFCSSVMHEALHNYH-QQRSLSLSPGVGGGGGGGGGS 244					
Db	63 SGHYATISLITV-SGAWAK-QMFTCRVAHTPSSTDWDNKTPSVC----- 105					
Qy	245 GGGGFTPTTKVILQSSCDGGHFPPTQLLCLVSGYTPGTINITWLEDGQVMDVLDSTA 304					
Db	106 --SRDFTPTTKVILQSSCDGGHFPPTQLLCLVSGYTPGTINITWLEDGQVMDVLDSTA 163					
Qy	305 STTQGEELASTOSELTLQKHLSDRTYTCQVYQCHTFEDSTKCCADSNPRGVSAYLSR 364					
Db	164 STTQGEELASTOSELTLQKHLSDRTYTCQVYQCHTFEDSTKCCADSNPRGVSAYLSR 223					
Qy	365 PSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASKGFPVNHSTRKEEQKQNGTLTVTST 424					
Db	224 PSPFDLFIKSPITITCLVVDLAPSKGTVNLWTSRASKGFPVNHSTRKEEQKQNGTLTVTST 283					
Qy	425 LPVGRDWEGETYQCRVTHPLRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTL 484					

CC or lyophilized form of target Ig derived protein; and a method for
CC producing an isolated mammalian target Ig derived protein. The target Ig
CC derived protein is useful in preparing a composition for diagnosing or
CC treating a target related condition in a cell, tissue, organ or animal,
CC e.g. tumor. This is the amino acid sequence of variable heavy chain
CC region Igs. Note: This sequence differs from the version given in SEQ ID
CC NO 35 in which the X residues have not been expanded to represent the
CC whole CDR regions.
XX
SQ Sequence 497 AA;

Query Match 57.3%; Score 1754.5; DB 9; Length 497;
Best Local Similarity 77.5%; Pred. No. 1.2e-112;
Matches 347; Conservative 17; Mismatches 57; Indels 27; Gaps 8;
Qy 129 REPQVYLPSPRDELTKNQVSLT--CLVKGFPYPSDIAVEWESNGQPENNYKTP-PVLDLS 185
Db 4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMTWDT-GSLNGTMTLTPATTLTL 62
Qy 186 VGSFFLYSLTVDKSRWQGNVFCSSVMHEALHNHY-QQRSLSLSPCKVEGGGGGGGS 244
Db 63 SGHYATISLTV-SGAWAK-QMFTCRVAHPSPSTDWVDNKTF SVC----- 105
Qy 245 GGGGSPFTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVDLSTA 304
Db 106 --SRDFTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVDLSTA 163
Qy 305 STTQEGELASTQSELTLISQKHWLSDRYTCQVYQGHTFEDSTKCADSNPRGVSYLSR 364
Db 164 STTQEGELASTQSELTLISQKHWLSDRYTCQVYQGHTFEDSTKCADSNPRGVSYLSR 223
Qy 365 PSPDLPFRKSPITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTVTST 424
Db 224 PSPDLPFRKSPITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTVTST 283
Qy 425 LPVGTDRWIEGETYQCRVTHPHLPALMRSTTKTS---GPRAAPEVYAFATPEWPGSRDK 481
Db 284 LPVGTDRWIEGETYQCRVTHPHLPALMRSTTKTS---GPRAAPEVYAFATPEWPGSRDK 343
Qy 482 RTLACLIONPMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQK 541
Db 344 RTLACLIONPMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQK 403
Qy 542 DEFICRAVHEAASPSQTVQRAVSNPCK 569
Db 404 DEFICRAVHEAASPSQTVQRAVSNPCK 431

Search completed: November 30, 2005, 00:28:31
Job time : 192 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:16:42 ; Search time 42 seconds
(without alignments)

1303.508 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHCPCPAPPELL.....HEAAPSQTVQRAVSNVPGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1766	57.7	428	1	EHHU		Ig epsilon chain C
2	1705.5	55.7	426	2	I36948		Ig epsilon-chain -
3	1225	40.0	330	1	GHU		Ig gamma-1 chain C
4	1219	39.8	374	2	S69339		Ig heavy chain V r
5	1217	39.8	255	4	S31866		Ig gamma-1 chain C
6	1172	38.3	234	2	PT0207		Ig gamma chain C r
7	1138	37.2	377	2	A23511		Ig gamma-3 chain C
8	1136	37.1	377	2	A60764		Ig gamma-3 chain C
9	1123	36.7	289	1	G3HUW1		Ig gamma-2 heavy c
10	1107	36.2	326	1	G2HU		Ig gamma-2 chain C
11	1097	35.8	327	1	G4HU		Ig gamma-4 chain C
12	883	28.9	323	1	GHRB		Ig gamma chain C r
13	868.5	28.4	328	2	I47160		Ig gamma 2b chain
14	868.5	28.4	328	2	I47159		Ig gamma 2a chain
15	865	28.3	327	2	I47162		Ig gamma 4 chain c
16	862.5	28.2	429	1	EHRT		Ig epsilon chain C
17	858	28.0	329	1	G2GP		Ig gamma-2 chain c
18	847.5	27.7	328	2	I47158		Ig gamma 1 chain c
19	840.5	27.5	328	2	I47161		Ig gamma 3 chain c
20	834.5	27.3	548	2	S38864		Ig epsilon chain C
21	820	26.8	470	2	S22080		Ig heavy chain pre
22	813	26.6	333	2	PS0018		Ig gamma-2b chain
23	812.5	26.6	329	1	G3MSC		Ig gamma-3 chain C
24	811.5	26.5	308	2	C30554		Ig heavy chain C r
25	811.5	26.5	472	2	S31459		Ig gamma-1 chain -
26	801.5	26.2	398	1	G3MSM		Ig gamma-3 chain C
27	794.5	26.0	444	2	PC4436		monoclonal antibod
28	789.5	25.8	324	1	GLMS		Ig gamma-1 chain C
29	784.5	25.6	326	2	PS0017		Ig gamma-1 chain C

RESULT 1

EHHU

Ig epsilon chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004

C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46

R;Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene

A;Reference number: A22771; MUID:84236029; PMID:6234164

A;Accession: A22771

A;Molecule type: DNA

A;Residues: 1-428 <FLA>

A;Cross-references: UNIPROT:P01854; UNIPARC:UPI000004BB48; GB:L00022; GB:J00227; GB:V005

R;Ueda, S.; Nakai, S.; Mishida, Y.; Hisajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog

A;Reference number: A23195; MUID:84207910; PMID:6327276

A;Accession: A23195

A;Molecule type: DNA

A;Residues: 2-428 <UED>

A;Cross-references: UNIPARC:UPI0000173783; GB:J00222; NID:g184755

R;Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992

A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing

A;Reference number: PH1214; MUID:92308839; PMID:1613458

A;Accession: PH1214

A;Molecule type: DNA

A;Residues: 320-428 <ZHA>

A;Cross-references: UNIPARC:UPI000014452D; EMBL:X63693; GB:S38668; NID:g32987

R;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Saeada, R.; Igarashi, K.; Kikuchi, M.; Sug

Nucleic Acids Res. 11, 719-726, 1983

A;Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha

A;Reference number: A93491; MUID:83168897; PMID:6300763

A;Accession: A93491

A;Molecule type: mRNA

A;Residues: 1-428 <SEN>

A;Cross-references: UNIPARC:UPI000004BB48; GB:L00022; GB:J00227; GB:V00555; NID:g185035

R;Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.

Cell 29, 691-699, 1982

A;Title: Duplication and deletion in the human immunoglobulin epsilon genes.

A;Reference number: A90824; MUID:83001945; PMID:6288268

A;Accession: A90824

A;Molecule type: DNA

A;Residues: 1-358, 'L', 360-428 <MAX>

A;Cross-references: UNIPARC:UPI0000173784; GB:J00222; NID:g184755

A;Note: this sequence difference may be due to polymorphism

R;Pennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-1

A;Reference number: A94418

A;Accession: A94418

A;Molecule type: protein

A;Residues: 'GAWTL' 6, 'X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 124
A;Cross-references: UNIPARC:UPI00000173785
A;Experimental source: myeloma protein Nd
R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A;Reference number: A93933; MUID:8305234; PMID:6815656
A;Accession: B93933
A;Molecule type: mRNA
A;Residues: 1-40;68-114;427-428 <KEN>
A;Cross-references: UNIPARC:UPI00001592FD; UNIPARC:UPI0000173786; UNIPARC:UPI0000173787;
R;Ikayama, S.
FEBS Lett. 224, 306-310, 1987
A;Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment
A;Reference number: S02438; MUID:88083554; PMID:3121387
A;Accession: S02438
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 98-352 <IKE>
A;Cross-references: UNIPARC:UPI0000173788
R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: A53116
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 320-428 <ZH2>
A;Cross-references: UNIPARC:UPI000014452D
A;Experimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIPI:141702)
R;Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A;Reference number: A46536; MUID:93122085; PMID:8419166
A;Accession: C46536
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 382-426 <HEL>
A;Cross-references: UNIPARC:UPI0000113EF7; GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIPI:125297)
A;Accession: D46536
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 382-391 <HE2>
A;Cross-references: UNIPARC:UPI0000113EF8; GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIPI:125299)
A;Accession: A46536
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 401-428 <HE3>
A;Cross-references: UNIPARC:UPI0000113EF5; GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIPI:123483)
C;Genetics:
A;Gene: GDB:IGHE
A;Cross-references: GDB:119335; OMIM:147180
A;Map position: 14q32.33-14q32.33
A;Introns: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
A;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul
F;22-87/Domain: immunoglobulin homology <IM1>
F;128-195/Domain: immunoglobulin homology <IM2>
F;232-301/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM4>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F;21,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;121,209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 57.7%; Score 1766; DB 1; Length 428;
Best Local Similarity 78.0%; Pred. No. 4.2e-102;
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;
QY 129 REPQVYTLPPSRDELTKNOVSLT--CLVKGFPSPDIAVEWESNGQPPENNYKTP-PVLDS 185
DB 4 QPSVFPLTRCCKNIPSNATSVTLGLATGYFPEPVMTWDT-GSLNGTTMTLPAATLTL 62
QY 186 VGSFFLYSLKLTVDKSRWQGNVFSVMEALHNHY-QORSLSLSPKVEGGGGGGGS 244
DB 63 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSDWDVNDKTF SVC----- 105
QY 245 GGGGSPPTPVTKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEQVMDVLDSTA 304
DB 106 --SRDFTPTPVTKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEQVMDVLDSTA 163
QY 305 STTQEGELASTOSELTLKOKHWSLSDRTYTCQVTYQGHTEFEDSTKKCADSNPRGVSAYLSR 364
DB 164 STTQEGELASTOSELTLKOKHWSLSDRTYTCQVTYQGHTEFEDSTKKCADSNPRGVSAYLSR 223
QY 365 PGPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKQKNGTLTWIST 424
DB 224 PGPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKQKNGTLTWIST 283
QY 425 LPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
DB 284 LPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343
QY 485 ACLIQNFMPEDISVQWLHNEVOLPDARHSTTTPRKTKGSGFFVFSRLEVTBRAWEQKDEF 544
DB 344 ACLIQNFMPEDISVQWLHNEVOLPDARHSTTTPRKTKGSGFFVFSRLEVTBRAWEQKDEF 403
QY 545 ICRVHEAAASPSQTVQRAVSVNPGK 569
DB 404 ICRVHEAAASPSQTVQRAVSVNPGK 428
RESULT 2
I36948
IG epsilon-chain - chimpanzee (fragment)
A;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
R;Accession: I36948
R;Sakoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan
A;Reference number: I36948; MUID:87147196; PMID:3103123
A;Accession: I36948
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-426 <RES>
A;Cross-references: UNIPARC:UPI000011754A; GB:M15398; NID:gi76797; PIDN:AAA35416.1; PID:gi
A;Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology <IM>
Query Match 55.7%; Score 1705.5; DB 2; Length 426;
Best Local Similarity 76.0%; Pred. No. 2.3e-98;
Matches 338; Conservative 20; Mismatches 62; Indels 25; Gaps 8;
QY 129 REPQVYTLPPSRDELTKNOVSLT--CLVKGFPSPDIAVEWESNGQPPENNYKTP-PVLDS 185
DB 3 RSPSLFPLTRCCKNIPSNATSVTLGLAMGYFPEPVMTWDA-GSLNGTTMTLPAATLTP 61
QY 186 VGSFFLYSLKLTVDKSRWQGNVFSVMEALHNHY-QORSLSLSPKVEGGGGGGGS 244
DB 62 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSDWDVNDKTF SVC----- 104
QY 245 GGGGSPPTPVTKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEQVMDVLDSTA 304
DB 105 --SRDFT-PTVTKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEQVMDVLDSTA 161

Qy 305 STTOGELASTOSTELTISOKHLSDRYTTCOVYQGHTEFSTKKCADSNPRGVSAYLSR 364
 Db 162 SATOGEELASTOSELTISOKHLSDRYTTCOVYQGHTEFSTKKCADSNPRGVSAYLSR 221
 Qy 365 PSPFDLFRKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTVTST 424
 Db 222 PSPFDLFRKSPPTITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTVTST 281
 Qy 425 LPVGTROWIEGTQCRVTHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTL 484
 Db 282 LPVGTROWIEGTQCRVTHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTL 341
 Qy 485 ACLIQNFWPEDISVQWLHNEVQLDARHSTTQPKTKSGGFFVFSRLVETRAEWEQKDEF 544
 Db 342 ACLIQNFWPEDISVQWLHNEVQLDARHSTTQPKTKSGGFFVFSRLVETRAEWEQKDEF 401
 Qy 545 ICRAVHEAAPSQTQRAVSVPNGK 569
 Db 402 ICRAVHEAAPSQTQRAVSVPNGK 426
 RESULT 3
 GHU
 Ig gamma-1 chain C region - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
 C:Accession: A93433; S33861; S33887; B90563; A90564; B91668; A91723; A02146
 R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
 Nucleic Acids Res. 10, 4071-4079, 1982
 A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
 A:Reference number: A93433; MUID:82274238; PMID:6287432
 A:Accession: A93433
 A:Molecule type: DNA
 A:Residues: 1-330 <ELL>
 A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370
 A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
 A:Note: Lys-330 is removed after translation
 R:Harris, L.J.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S33904
 A:Accession: S36861
 A:Molecule type: DNA
 A:Residues: 2-330 <HAR>
 A:Cross-references: UNIPARC:UPI000013C0FE; EMBL:Z17370
 R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
 Cell 29, 671-679, 1982
 A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
 A:Reference number: S33887; MUID:83001943; PMID:6811139
 A:Accession: S33887
 A:Molecule type: DNA
 A:Residues: 88-113;235-330 <TAK>
 A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
 R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
 Biochemistry 9, 3161-3170, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
 A:Reference number: A90563; MUID:71064024; PMID:5489771
 A:Contents: myeloma protein Eu
 A:Accession: B90563
 A:Molecule type: protein
 A:Residues: 1-96, R', 98-135 <CUN>
 A:Cross-references: UNIPARC:UPI000017378D
 A:Note: this sequence has the G1m(3) marker, 97-Arg
 R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
 A:Reference number: A90564; MUID:71064025; PMID:5530842
 A:Contents: Eu
 A:Accession: A90564
 A:Molecule type: protein
 A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
 A:Cross-references: UNIPARC:UPI000017378E
 A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie) i
 igen Primaerstruktur.
 A:Reference number: A91668; MUID:77070269; PMID:826475
 A:Contents: myeloma protein Nie
 A:Accession: B91668
 A:Molecule type: protein
 A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 273
 A:Cross-references: UNIPARC:UPI000017378F
 A:Note: this sequence has the G1m(17) and G1m(1) markers
 R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
 A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 Ko1
 A:Reference number: A91723; MUID:83289131; PMID:6884994
 A:Contents: myeloma protein KO1; disulfide bonds
 A:Accession: A91723
 A:Molecule type: protein
 A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
 A:Cross-references: UNIPARC:UPI0000173790
 A:Note: this sequence has the G1m(3) and G1m(non-1) markers
 R;Gall, W.E.; Edelman, G.M.
 Biochemistry 9, 3188-3196, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
 A:Reference number: A90565; MUID:71064027; PMID:4923144
 A:Contents: annotation; disulfide bonds
 R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
 A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
 enamide cleavage products, and the disulfide bridges.
 A:Reference number: A91667; MUID:77070267; PMID:1002129
 A:Contents: annotation; disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG1
 A:Cross-references: GDB:120085; OMIM:147100
 A:Map position: 14q32.33-14q32.33
 A:Introns: 99/1; 114/1; 224/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 14
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:137-206/Domain: immunoglobulin homology <IM2>
 F:243-310/Domain: immunoglobulin homology <IM3>
 F:27-83 144-204, 250-308/Disulfide bonds: #status experimental
 F:103/Disulfide bonds: interchain (to light chain) #status experimental
 F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 40.0%; Score 1225; DB 1; Length 330;
 Best Local Similarity 97.0%; Pred. No. 9.6e-69;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 60
 Db 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPPKDRLMISRTPEVTCVVVDVSHEDPEVKF 158
 Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
 Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 Db 219 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
 Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFSCSMHEALHNHYTQKSLSLSPGK 232
 Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFSCSMHEALHNHYTQKSLSLSPGK 330
 RESULT 4
 S69339
 Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 39.8%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 2.6e-68;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 143 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 203 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 262
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 263 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 322
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 323 PVLDSGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSFGK 374

RESULT 5
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PII
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 39.8%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 2.2e-68;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 24 ESKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 84 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 143

C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 39.8%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 2.6e-68;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 143 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 203 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 262
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 263 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 322
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 323 PVLDSGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSFGK 374

RESULT 5
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PII
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 39.8%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 2.2e-68;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 24 ESKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 84 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 143

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 144 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 203
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 204 PVLDSGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSFGK 255

RESULT 6

PT0207
Ig gamma chain C region - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C;Accession: PT0207
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207; MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Molecule type: mRNA
A;Residues: 1-234 <EHR>
A;Cross-references: UNIPARC:UPI0000176F05
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 1172; DB 2; Length 234;
Best Local Similarity 95.6%; Pred. No. 1.2e-65;
Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 10 EPKSCDTHTTCTCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 69
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 70 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 129
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 130 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 189

RESULT 7

A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27272
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 37.2%; Score 1138; DB 2; Length 377;

Best Local Similarity 89.7%; Pred. No. 2.8e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 60
Db 146 EPKSCDTPPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 205

Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 206 KWIYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 265

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 266 ISKTKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 325

Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVPCFVSVHMEALHNHYQOQSLSLSPGK 232
Db 326 PVLDSGSGFFLYSKLTVDKSRWQQGNVPCFVSVHMEALHNHYQOQSLSLSPGK 377

RESULT 8
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 37.1%; Score 1136; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 3.7e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 60
Db 146 EPKSCDTPPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 205

Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 206 KWIYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 265

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 266 ISKTKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 325

Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVPCFVSVHMEALHNHYQOQSLSLSPGK 232
Db 326 PVLDSGSGFFLYSKLTVDKSRWQQGNVPCFVSVHMEALHNHYQOQSLSLSPGK 377

RESULT 9
G3HUM1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy
A:Reference number: A90442; MUID:81021548; PMID:677477
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein

A:Residues: 1-289 <FRA>
A:Cross-references: UNIPARC:UPI0000173797
A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain,
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A:Reference number: A92219; MUID:77118561; PMID:402363
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A:Cross-references: UNIPARC:UPI0000173798
A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamm
idue segment (12-28)
A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A:Cross-references: UNIPARC:UPI0000173799
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R:Alexander, A.; Steinmetz, M.; Barrittault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A:Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C
A:Note: a carboxyl-terminal Lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 36.7%; Score 1123; DB 1; Length 289;
Best Local Similarity 88.3%; Pred. No. 1.7e-62;
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 60
Db 59 EPKSCDTPPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 118

Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 119 KWIYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 178

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 179 ISKTKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 238

Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVPCFVSVHMEALHNHYQOQSLSLSPG 231
Db 239 PVLDSGSGFFLYSKLTVDKSRWQQGNVPCFVSVHMEALHNHYQOQSLSLSPG 289

RESULT 10
G2HU
Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)
 C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
 C;Accession: A93906; A92809; A90752; A93132; A02148
 R;Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
 A;Reference number: A93906; MUID:82197621; PMID:680498
 A;Accession: A93906
 A;Molecule type: DNA
 A;Residues: 1-326 <ELL>
 A;Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:G32
 A;Note: Lys-326 is probably removed posttranslationally
 R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
 J. Immunol. 125, 1048-1054, 1980
 A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
 A;Reference number: A92809; MUID:81007873; PMID:6774012
 A;Contents: myeloma protein Til
 A;Accession: A92809
 A;Molecule type: protein
 A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
 A;Cross-references: UNIPARC:UPI0000173791
 A;Note: Trp-156 is at or near the complement-binding site
 R;Connell, G.E.; Parr, D.M.; Hofmann, T.
 Can. J. Biochem. 57, 758-767, 1979
 A;Title: The amino acid sequences of the three heavy chain constant region domains of a
 A;Reference number: A90752; MUID:80001357; PMID:113060
 A;Contents: myeloma protein Zie
 A;Accession: A90752
 A;Molecule type: protein
 A;Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
 A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
 A;Note: this sequence has since been revised
 R;Hofmann, T.; Parr, D.M.
 Mol. Immunol. 16, 923-925, 1979
 A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G
 A;Reference number: A93132; MUID:80114419; PMID:118920
 A;Contents: Zie
 A;Accession: A93132
 A;Molecule type: protein
 A;Residues: 238-275 <HOF>
 A;Cross-references: UNIPARC:UPI0000173794
 R;Hofmann, T.; Parr, D.M.
 submitted to the Atlas, March 1980
 A;Reference number: A94591
 A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
 A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
 ned
 R;Milstein, C.; Frangione, B.
 Biochem. J. 121, 217-225, 1971
 A;Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
 A;Reference number: A90253; MUID:72033500; PMID:4940472
 A;Contents: annotation; myeloma protein Sa, disulfide bonds
 R;Frangione, B.; Milstein, C.; Pink, J.R.L.
 Nature 221, 145-148, 1969
 A;Title: Structural studies of immunoglobulin G.
 A;Reference number: A93157; MUID:69064124; PMID:5782707
 A;Contents: annotation; Sa, disulfide bonds
 C;Genetics:
 A;Gene: IGHC2
 A;Cross-references: GDB:119338; OMIM:147110
 A;Map position: 14q23.33-14q32.33
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM1>
 F;133-202/Domain: immunoglobulin homology <IM2>
 F;239-306/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83,140-200,246-304/Disulfide bonds: #status experimental
 F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.2%; Score 1107; DB 1; Length 326;
 Best Local Similarity 88.4%; Pred. No. 1.9e-61;
 Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;
 1 EPKSCDKTHTCPCPAPELLLGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 99 ERKCCVE---CPCCAPP-VAGPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 154
 61 NMYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQNMNMGKEYCKVSKNSKALPAPIETK 120
 155 NMYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQDMLNGKEYCKVSKNSKGLPAPIETK 214
 121 ISKAKVORPEPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIADVESNGQPNVKKTPP 180
 215 ISKTKGQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFPSPDIADVESNGQPNVKKTPP 274
 181 PVLDSVGSGFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTKQSLSLSPGK 232
 275 PMLDSGSGFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTKQSLSLSPGK 326
 RESULT 11
 G4HU
 IG gamma-4 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
 C;Accession: A90933; A90249; A02150
 R;Ellison, J.; Buxbaum, J.; Hood, L.
 DNA 1, 11-18, 1981
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A;Reference number: A90933; MUID:83157104; PMID:6299662
 A;Accession: A90933
 A;Molecule type: DNA
 A;Residues: 1-327 <ELL>
 A;Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
 A;Note: the sequence was determined from the germline gene
 R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
 Biochem. J. 117, 33-47, 1970
 A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re
 A;Reference number: A90249; MUID:70207560; PMID:4192699
 A;Accession: A90249
 A;Molecule type: protein
 A;Residues: 1-30;81-326 <PIN>
 A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
 C;Genetics:
 A;Gene: GDB:IGHG4
 A;Cross-references: GDB:119340; OMIM:147130
 A;Map position: 14q32.33-14q32.33
 A;Introns: 99/1; 111/1; 221/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM1>
 F;99-110/Region: hinge
 F;134-203/Domain: immunoglobulin homology <IM2>
 F;240-307/Domain: immunoglobulin homology <IM3>
 F;14/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83,141-201,247-305/Disulfide bonds: #status predicted
 F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 35.8%; Score 1097; DB 1; Length 327;
 Best Local Similarity 90.5%; Pred. No. 8e-61;
 Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 11 CPCCPAPELLGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNVDGVEVH 70
 106 CPSCPAPEFLGSPSVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNVDGVEVH 165
 71 NVKTKPREQYNSTYRVVSVLTVLHQNMNMGKEYCKVSKNSKALPAPIETKISKAVQPRE 130
 166 NAKTKPREQYNSTYRVVSVLTVLHQDMLNGKEYCKVSKNSKGLPSSIEKISKAKQPRE 225

QY 131 PQVYTLPPSRDELTKNOVSLTCLVKGYPSDIAVEWESNGOPENNYKTTTPVLDVSGSFF 190
DB 226 PQVYTLPPSQEEMTKNQVSLTCLVKGYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFF 285
QY 191 LYSKLTVDKSRWQGNVFCSSVMHEALHNHYQOQSLSLSPK 232
DB 286 LYSRLTVDKSRWQGNVFCSSVMHEALHNHYQOQSLSLSPK 327

RESULT 12
GHRB
Ig gamma chain C region - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot
A:Reference number: A91749; MUID:84030930; PMID:6313520
A:Accession: A91749
A:Molecule type: mRNA
A:Residues: 1-323 <BER>
A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R:Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A:Reference number: A90290; MUID:76135469; PMID:1243651
A:Accession: A90290
A:Molecule type: protein
A:Residues: 1-47, 'E', '49-71', 'PV', '72-128' <PRA>
A:Cross-references: UNIPARC:UPI00001737AB
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A:Reference number: A93928; MUID:83299917; PMID:6193512
A:Accession: A93928
A:Molecule type: mRNA
A:Residues: 88-103, 'M', '105-143', 'E', '145-184', 'A', '186', 'E', '188-266' <MAR>
A:Cross-references: UNIPARC:UPI000165ED; GB:M16426; NID:G165111; PIDN:AAA31289.1; PID:
A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic mark
R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
A:Reference number: A90245; MUID:70110015; PMID:5461106
A:Accession: A90245
A:Molecule type: protein
A:Residues: 132-143, 'E', '145-161' <FRU>
A:Cross-references: UNIPARC:UPI00001737AC
R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A:Reference number: A94416
A:Accession: A94416
A:Molecule type: protein
A:Residues: 129-131; 155-172, 'D', '174-184', 'A', '186', 'E', '188-200', 'D', '202-217', 'E', '219-232', 'Q',
A:Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE
A:Note: this has the e15 allotypic marker, 185-Ala
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-82/Domain: immunoglobulin homology <IM1>
F:130-199/Domain: immunoglobulin homology <IM2>
F:236-303/Domain: immunoglobulin homology <IM3>
F:173/Binding site: carbohydrate (Asn) #status predicted

Query Match 28.9%; Score 883; DB 1; Length 323;
Best Local Similarity 64.5%; Pred. No. 1.4e-47;
Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;
QY 1 EPKSCDKTH-----TC--PPCPAPELLGGPSVFLPPPKDITLMISRTPEV 44
: : : : : |

DB 76 QPVTGNVAHPATNTKVDKTVAPSTCSPKTCPPPELLGGPSVFIAPPKDKDTLMISRTPEV 135
QY 45 TCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQNTSTYRVVSVLTVTLQHWMMNGKEY 104
DB 136 TCVVVDVSDDDPEVQFTWVNNQVTRAPPLAEQQFNSTIRVVSTLPIHQDWLGRKEF 195
QY 105 KCKVSNKALPAPIEKTISKAKVQPRQPQVYTLPPSRDELTKNQVSLTCLVKGYFSPVSDIAV 164
DB 196 KCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPREEELSRSLTCTMNGFYFSPDISV 255
QY 165 EWESNGOPENNYKTTTPVLDVSGSFFLYSKLTVDKSRWQGNVFCSSVMHEALHNHYQOQ 224
DB 256 EWEKNGKAEDNYKITTPAVLDSDGSIYFLNKLSTVPTSEWQKQDVFVTCSSVMHEALHNHYTQK 315
QY 225 SLSLSPK 232
DB 316 SISRSPK 323

RESULT 13
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:G433125; PIDN:AAAS2218.1; PI:
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 28.4%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 1.1e-46;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;
QY 11 CPPCPAPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70
DB 106 CPICPACE-SFGPSVFIAPPKDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164
QY 71 NVKTKPREEQYNSTYRVVSVLTVTLQHWMMNGKYKCKVSNKALPAPIEKTISKAKVQPRE 130
DB 165 TAQTRPKEEQFNSTYRVVSVLPIHQDWLNGKEFKCKVNNKDLPAPIRIISKAKGQTR 224
QY 131 PQVYTLPPSRDELTKNQVSLTCLVKGYFSPVSDIAVEWESNGO--PENNYKTTTPVLDVSGS 188
DB 225 PQVYTLPPHAEELSRSKVSITCLVIGFYPPDIDVEWQKQGPPEPEGNVTRITTPQDQVDGT 284
QY 189 FFYLSKLTVDKSRWQGNVFCSSVMHEALHNHYQOQSLSLSPK 232
DB 285 YFLYSKFSVDKASQSGGIFQCAVWHEALHNHYTQKSISKTPGK 328

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:15:42 ; Search time 229 Seconds

(without alignments)
1753.038 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHTCPCPAPPELL.....HEAAPSQTVORAVSNPGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1766	57.7	428	1 IGHE HUMAN	P01854 homo sapien
2	1225	40.0	330	1 IGHG1 HUMAN	P01857 homo sapien
3	1225	40.0	465	2 Q6GMX6 HUMAN	Q6gmx6 homo sapien
4	1225	40.0	466	2 Q6IN78 HUMAN	Q6in78 homo sapien
5	1225	40.0	469	2 Q569F4 HUMAN	Q569f4 homo sapien
6	1225	40.0	469	2 Q727P5 HUMAN	Q727p5 homo sapien
7	1225	40.0	470	2 Q725W1 HUMAN	Q725w1 homo sapien
8	1225	40.0	470	2 Q6FJA4 HUMAN	Q6fja4 homo sapien
9	1225	40.0	472	2 Q6N089 HUMAN	Q6n089 homo sapien
10	1225	40.0	475	2 Q5EFES HUMAN	Q5efes homo sapien
11	1225	40.0	475	2 Q6GMW7 HUMAN	Q6gmw7 homo sapien
12	1225	40.0	476	2 Q6GMX1 HUMAN	Q6gmx1 homo sapien
13	1225	40.0	679	2 Q6FPQ8 HUMAN	Q6fpq8 homo sapien
14	1221	39.9	473	2 Q6P055 HUMAN	Q6p055 homo sapien
15	1221	39.9	475	2 Q6MZQ6 HUMAN	Q6mzq6 homo sapien
16	1221	39.9	480	2 Q6N094 HUMAN	Q6n094 homo sapien
17	1221	39.9	481	2 Q6N097 HUMAN	Q6n097 homo sapien
18	1221	39.9	482	2 Q72351 HUMAN	Q72351 homo sapien
19	1219	39.8	348	2 Q6PYX1 HUMAN	Q6pyx1 homo sapien
20	1219	39.8	473	2 Q6MZV7 HUMAN	Q6mzv7 homo sapien
21	1219	39.8	478	2 Q6P181 HUMAN	Q6p181 homo sapien
22	1219	39.8	480	2 Q6PJF1 HUMAN	Q6pjf1 homo sapien
23	1218	39.8	466	2 Q6N096 HUMAN	Q6n096 homo sapien
24	1214	39.7	475	2 Q6N095 HUMAN	Q6n095 homo sapien
25	1214	39.7	544	2 Q6FJ95 HUMAN	Q6fj95 homo sapien
26	1196	39.1	487	2 Q65ZL2 9MURI	Q65z12 mus sp. f/v
27	1164	38.0	475	2 Q5RE17 PONPY	Q5re17 porogo pygma
28	1138	37.2	354	2 Q6FTT2 HUMAN	Q6ftt2 homo sapien
29	1138	37.2	518	2 Q6N030 HUMAN	Q6n030 homo sapien
30	1138	37.2	519	2 Q5EBM2 HUMAN	Q5ebm2 homo sapien
31	1134	37.1	521	2 Q8N4Y9 HUMAN	Q8n4y9 homo sapien

RESULT 1				
IGHE HUMAN				
ID	IGHE HUMAN	STANDARD;	PRT;	428 AA.
AC	P01854;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig epsilon chain C region.			
GN	Name=IGHE;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	MEDLINE=83168897; PubMed=6300763;			
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,			
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;			
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin			
RT	epsilon chain cDNA.";			
RL	Nucleic Acids Res. 11:719-726(1983).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, AND VARIANT LEU-359.			
RA	MEDLINE=83001945; PubMed=6288268; DOI=10.1016/0092-8674(82)90185-4;			
RA	Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;			
RT	"Duplication and deletion in the human immunoglobulin epsilon genes.";			
RL	Cell 29:691-699(1982).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RA	MEDLINE=84236029; PubMed=6234164;			
RA	Planagan J.G., Rabbitts T.H.;			
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant			
RT	region gene, and evidence for three non-allelic genes.";			
RL	EMBO J. 1:655-660(1982).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RA	MEDLINE=84207910; PubMed=6327276;			
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;			
RT	"Long terminal repeat-like elements flank a human immunoglobulin			
RT	epsilon pseudogene that lacks introns.";			
RL	EMBO J. 1:1539-1544 (1982).			
RN	[5]			
RP	PRELIMINARY PROTEIN SEQUENCE (MYELOMA PROTEIN ND).			
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;			
RL	(In) Bach M.K. (eds.);			
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,			
RL	Marcel Dekker, New York (1978).			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE OF 1-40; 68-114 AND 427-428.			
RA	MEDLINE=83065234; PubMed=6815656;			
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,			
RA	Bell L.O., Gould H.J.;			
RT	"Cloning and sequence determination of the gene for the human			

P01860 homo sapien
Q8nf17 homo sapien
P01859 homo sapien
Q6n093 homo sapien
Q6mzu6 homo sapien
Q6p6e4 homo sapien
P01861 homo sapien
Q8tc63 homo sapien
Q68cn4 homo sapien
Q6mzx7 homo sapien
P01870 oryctolagus
Q95m34 equus cabal
P01855 rattus norv
P01862 cavia porce

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=92274238; PubMed=6287432;
RX Ellison J.W.; Berson B.J.; Hood L.E.;
RA "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RT Nucleic Acids Res. 10:4071-4079(1982).
RL (2)
RN PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RP MEDLINE=71064024; PubMed=5489771;
RX Cunningham B.A.; Rutishauser U.; Gall W.E.; Gottlieb P.D.;
RA Waxdal M.J.; Edelman G.M.;
RA "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid covalence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN (3)
RN PROTEIN SEQUENCE OF 136-329 (EU).
RP MEDLINE=71064025; PubMed=5530842;
RX Rutishauser U.; Cunningham B.A.; Bennett C.; Konigsberg W.H.;
RA Edelman G.M.;
RA "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN (4)
RN PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
RP MEDLINE=77070269; PubMed=826475;
RX Ponstingl H.; Hilschmann N.;
RA "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN (5)
RN PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RP MEDLINE=83289131; PubMed=6884994;
RX Schmidt W.E.; Jung H.-D.; Palm W.; Hilschmann N.;
RA "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN (6)
RN DISULFIDE BONDS.
RP MEDLINE=71064027; PubMed=4923144;
RX Gall W.E.; Edelman G.M.;
RA "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds";
RL Biochemistry 9:3188-3196(1970).
RN (7)
RN DISULFIDE BONDS.
RP MEDLINE=77070267; PubMed=1002129;
RX Dreker L.; Schwarz J.; Reichel W.; Hilschmann N.;
RA "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN (8)
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP MEDLINE=81208100; PubMed=7236608;
RX Deisenhofer J.;
RA "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -!- MISCELLANEOUS: NIE has the G1M(17) allotypic marker, 97-K, and the

CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC G1M(3) marker and the G1M (non-1) markers.
CC -!- MISCELLANEOUS: NIE also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
DR PIR; A93433; GHHU.
DR PDB; 1AJ7; X-ray; H=1-103.
DR PDB; 1AQK; X-ray; H=1-103.
DR PDB; 1D5B; X-ray; B/H=1-101.
DR PDB; 1D51; X-ray; H=1-101.
DR PDB; 1D6V; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1H2H; X-ray; H/K=1-330.
DR PDB; 1I72; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1QQX; X-ray; A/B=119-330.
DR PDB; 1T83; X-ray; A/B=107-330.
DR PDB; 2RCS; X-ray; H=1-103.
DR HGNC; HGNC:5525; IGHG1.
DR MIM; 147100; .
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; C1-set; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
DR 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
FT REGION 1 98
FT REGION 99 110 Hinge.
FT REGION 111 223 CH2.
FT REGION 224 330 CH3.
FT CARBOHYD 180 180 N-linked (GlcNAc...).
FT DISULFID 27 83
FT DISULFID 103 103 Interchain (with light chain).
FT DISULFID 109 109 Interchain (with heavy chain).
FT DISULFID 112 112 Interchain (with heavy chain).
FT DISULFID 144 204
FT DISULFID 250 308
FT VARIANT 97 97
FT VARIANT 239 239 K -> R (in G1M(3) marker).
FT VARIANT 241 241 /FTID=VAR_003886.
FT NON_TER 1 1 D -> E (in G1M(non-1) marker).
FT STRAND 23 24 /FTID=VAR_003887.
FT STRAND 26 33 L -> M (in G1M(non-1) marker).
FT STRAND 38 38 /FTID=VAR_003888.
FT STRAND 41 41
FT TURN 42 45
FT TURN 48 49

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FT STRAND 50 52
FT STRAND 57 58
FT TURN 59 61
FT STRAND 62 71
FT HELIX 73 75
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FT STRAND 82 87
FT TURN 88 91
FT STRAND 92 97
FT TURN 102 103
FT STRAND 122 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 149
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 167
FT STRAND 171 172
FT STRAND 176 177
FT TURN 179 180
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
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FT TURN 209 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 245 256
FT STRAND 261 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 311
FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 40.0%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 1e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158

QY 61 NWTVDGVGVHNVKTPREEQYNSTYRVWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 159 NWTVDGVGVHNAKTPREEQYNSTYRVWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 218

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 219 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 278

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 279 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 330

RESULT 3
Q6GMX6_HUMAN
ID Q6GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

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DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -: mRNA.
GO; GO:0016021; C-integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 234 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293

QY 61 NWTVDGVGVHNVKTPREEQYNSTYRVWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 294 NWTVDGVGVHNAKTPREEQYNSTYRVWSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 353

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 354 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 413

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 414 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 465

RESULT 4

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Q6IN78 HUMAN
ID Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -; mRNA.
DR HSP; P01661; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50834 MW; 53EB0BCDE81076E CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 466;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 235 EPKSCDKTHCTCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 294
QY 61 NWYDGVGVHNVKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 295 NWYDGVGVHNVKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 354
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 355 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 414
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181 PVLDSDGSGFFLYSKLTVDKSRWQGNVFSQVHSCVMHEALHNHYQQRSLSPGK 232
181 PVLDSDGSGFFLYSKLTVDKSRWQGNVFSQVHSCVMHEALHNHYQQRSLSPGK 232
415 PVLDSDGSGFFLYSKLTVDKSRWQGNVFSQVHSCVMHEALHNHYQQRSLSPGK 466
415 PVLDSDGSGFFLYSKLTVDKSRWQGNVFSQVHSCVMHEALHNHYQQRSLSPGK 466

RESULT 5
Q569F4 HUMAN
ID Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human)
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 469;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 238 EPKSCDKTHCTCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 297
QY 61 NWYDGVGVHNVKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 298 NWYDGVGVHNVKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 357
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 358 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 417
QY 181 PVLDSDGSGFFLYSKLTVDKSRWQGNVFSQVHSCVMHEALHNHYQQRSLSPGK 232
418 PVLDSDGSGFFLYSKLTVDKSRWQGNVFSQVHSCVMHEALHNHYQQRSLSPGK 469

RESULT 6
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Db 359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKPTTP 418
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVSMHEALHNYHQRSLSLSPGK 232
Db 419 PVLDSGDSFFLYSKLTVDKSRWQGNVFSQVSMHEALHNYHQRSLSLSPGK 470

RESULT 8
Q6PJA4 HUMAN
ID Q6PJA4 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; 1ADO.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 239 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 298

RESULT 9
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fodor G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -; mRNA.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 472;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 241 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 300

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQNMNGKEYCKVKSNKALPAPIEKT 120
Db 301 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQNMNGKEYCKVKSNKALPAPIEKT 360

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKPTTP 180
Db 361 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKPTTP 420

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVSMHEALHNYHQRSLSLSPGK 232
Db 421 PVLDSGDSFFLYSKLTVDKSRWQGNVFSQVSMHEALHNYHQRSLSLSPGK 472

RESULT 10
```

Q5BFE5 HUMAN
ID Q5BFE5_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q5BFE5
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RL antibody T125";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY894992; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL. 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy
FT chain.
FT
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYDGVGVHNVKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 120
DB 304 NWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 363
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 423
QY 181 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 424 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 11
Q6GMW7 HUMAN
ID Q6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE5D736860F8 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYDGVGVHNVKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 120
DB 304 NWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 363
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 423
QY 181 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 424 PVLDSVGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 12
Q6GMX1 HUMAN
ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Mardina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Sutterch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPRO03599; IG.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03597; IG.C1.
DR InterPro; IPRO03006; IG.MHC.
DR InterPro; IPRO03596; IG.V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 476;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTPCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 245 EPKSCDKTHCTPCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 304

QY 61 NWYVDGVEVHNKTPRBEQYNSTYRVVSVLTVLHQDNMNGKEYKKCKVSNKALPAPIEKT 120
DB 305 NWYVDGVEVHNKTPRBEQYNSTYRVVSVLTVLHQDNMNGKEYKKCKVSNKALPAPIEKT 364

QY 121 ISKAVQREPOVYTLPPSRDELTKNQVSLTCLVGFPSDITAVESNGQPENNYKTP 180
DB 365 ISKAVQREPOVYTLPPSRDELTKNQVSLTCLVGFPSDITAVESNGQPENNYKTP 424

QY 181 PVLDSVGSFPLYSKLTVDKSRNQQGVFSCSVWHEALHNHYQOQSLSISPGK 232
DB 425 PVLDSVGSFPLYSKLTVDKSRNQQGVFSCSVWHEALHNHYQOQSLSISPGK 476

RESULT 13
Q96PQ8_HUMAN
ID Q96PQ8_HUMAN PRELIMINARY; PRT; 679 AA.

AC Q96PQ8;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Hu Z., Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272774; AAK58686.2; -; mRNA.
DR HSP; P08709; IKLI.
DR SMR; Q96PQ8; 39-180, 191-444, 447-679.
DR Ensembl; ENSG00000057593; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPRO00152; Asx hydroxyl_S.
DR InterPro; IPRO00742; EGF 2.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO01438; EGF_II.
DR InterPro; IPRO06209; EGF-like.
DR InterPro; IPRO02383; GLA blood.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03597; IG.C1.
DR InterPro; IPRO03006; IG.MHC.
DR InterPro; IPRO01314; Peptidase_S1A.
DR InterPro; IPRO01254; Peptidase_S1_S6.
DR InterPro; IPRO00294; VitK_dep_GLA.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFblood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS50026; EGF 3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA; 1; UNKNOWN_1.
DR PROSITE; PS50998; GLA 2; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 679;
Best Local Similarity 97.0%; Pred. No. 2.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTPCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
|||||
|||||

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Db 448 EPKSCDKTHTCCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 507
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT 120
Db 508 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 567
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 568 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 627
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 628 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 679

RESULT 14
Q6P055 HUMAN
ID Q6P055_HUMAN PRELIMINARY; PRT; 473 AA.
AC Q6P055
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;
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Query Match 39.9%; Score 1221; DB 2; Length 473;
Best Local Similarity 96.6%; Pred. No. 3e-74;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 242 EPKSCDKTHTCCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 301
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT 120
Db 302 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 361
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 362 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 421
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 422 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 473

RESULT 15
Q6MZQ6 HUMAN
ID Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weill B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 39.9%; Score 1221; DB 2; Length 475;
Best Local Similarity 96.6%; Pred. No. 3.1e-74;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 244 EPKSCDKTHTCCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT 120
Db 304 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 363
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
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Db 364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 423
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 424 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEGLNHYTQKSLSLSPGK 475

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Job time : 232 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:25:23 ; Search time 45 seconds
(without alignments)
1045.388 Million cell updates/sec

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Perfect score: 3060
Sequence: 1 EPRKCDKTHCPAPPELL.....HEAAPSQTQRAVSVNPGK 569

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707	55.8	331	2	US-09-401-636-1
2	1701	55.6	325	2	US-09-701-623C-1
3	1273.5	41.6	711	2	US-09-485-737B-90
4	1273.5	41.6	711	2	US-10-071-485-90
5	1247	40.8	277	2	US-09-428-082B-22
6	1243	40.6	268	2	US-09-428-082B-8
7	1243	40.6	269	2	US-09-422-838C-46
8	1232	40.3	660	2	US-09-181-706-8
9	1232	40.3	660	2	US-09-458-791-8
10	1232	40.3	660	2	US-09-459-066-8
11	1232	40.3	660	2	US-09-459-065-8
12	1229	40.2	379	2	US-10-679-999-9
13	1226	40.1	253	2	US-09-428-082B-16
14	1225	40.0	232	1	US-08-595-043A-50
15	1225	40.0	232	2	US-09-968-362A-26
16	1225	40.0	232	2	US-09-932-812A-26
17	1225	40.0	331	2	US-09-178-869-2
18	1225	40.0	331	2	US-09-761-413-2
19	1225	40.0	360	2	US-09-180-100-11
20	1225	40.0	360	2	US-09-949-713-11
21	1225	40.0	371	1	US-08-236-311-7
22	1225	40.0	371	2	US-08-457-918-7
23	1225	40.0	371	2	US-10-157-408-7
24	1225	40.0	376	2	US-09-180-100-22
25	1225	40.0	376	2	US-09-949-713-22
26	1225	40.0	396	1	US-08-784-512-3
27	1225	40.0	396	2	US-09-176-228-3

28	1225	40.0	424	4	PCT-US95-03866-12	Sequence 12, Appl
29	1225	40.0	424	4	PCT-US95-03866-14	Sequence 14, Appl
30	1225	40.0	437	4	PCT-US96-10043-11	Sequence 11, Appl
31	1225	40.0	442	2	US-08-472-888A-7	Sequence 7, Appl
32	1225	40.0	442	4	PCT-US96-10043-9	Sequence 9, Appl
33	1225	40.0	446	2	US-08-397-411-7	Sequence 7, Appl
34	1225	40.0	449	1	US-08-458-516-13	Sequence 13, Appl
35	1225	40.0	452	2	US-09-773-877B-16	Sequence 16, Appl
36	1225	40.0	459	1	US-08-157-101A-7	Sequence 7, Appl
37	1225	40.0	462	2	US-09-773-877B-18	Sequence 18, Appl
38	1225	40.0	467	2	US-08-030-175-41	Sequence 41, Appl
39	1225	40.0	467	2	US-08-030-175-42	Sequence 42, Appl
40	1225	40.0	470	2	US-10-104-047-3730	Sequence 3730, Ap
41	1225	40.0	475	2	US-09-740-002-27	Sequence 27, Appl
42	1225	40.0	476	1	US-08-378-939-10	Sequence 10, Appl
43	1225	40.0	476	2	US-08-487-550-4	Sequence 4, Appl
44	1225	40.0	476	2	US-08-487-550-12	Sequence 12, Appl
45	1225	40.0	476	2	US-09-526-098-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401.636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1

Query Match		55.8%	Score 1707;	DB 2;	Length 331;
Best Local Similarity		100.0%	Pred. No. 2e-136;		
Matches 320;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
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DB	12	FTPTVKILQSSCDGGHFPPTIQLLCIVSGYTGCTINITWLEDGQVMDVLDLSTASTTQE	71		
QY	310	GELASTQSELTLSQKHWLSDRITYCQVYQGHTEFDTSTKCADSNPRGVSAYLSRSPDP	369		
DB	72	GELASTQSELTLSQKHWLSDRITYCQVYQGHTEFDTSTKCADSNPRGVSAYLSRSPDP	131		
QY	370	LFIRKSPITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTITSLTPVGT	429		
DB	132	LFIRKSPITCLVVDLAPSKGTNLTWSRASKPVNHSRKEEKORNGTLTITSLTPVGT	191		
QY	430	RDWTEGYQCRVTHPLPRALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTLAQLIQ	489		
DB	192	RDWTEGYQCRVTHPLPRALMRSTTKTSGPRAPEVYAFATPEWPGSRDKRTLAQLIQ	251		
QY	490	NFMPEDISVQWLNHNEVQLPDARHSTQPRKTKGSGFFVFSRLVETRAEWEQKDEFTICRAV	549		
DB	252	NFMPEDISVQWLNHNEVQLPDARHSTQPRKTKGSGFFVFSRLVETRAEWEQKDEFTICRAV	311		
QY	550	HEAAPSQTQRAVSVNPGK	569		
DB	312	HEAAPSQTQRAVSVNPGK	331		

```
RESULT 2
US-09-701-623C-1
; Sequence 1, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 325
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: CH2CH3 of human IgE
; PUBLICATION INFORMATION:
; AUTHORS: Dorrington,
; JOURNAL: Immunology
; VOLUME: 41
; PAGES: 3-25
; DATE: 1978
US-09-701-623C-1

Query Match 55.6%; Score 1701; DB 2; Length 325;
Best Local Similarity 99.4%; Pred. No. 6.2e-136;
Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 250 FTPTVKILQSSDGGGHPPTTQLCLVSGYTPGINTIWLBDGQVMDVLDLSTATTQ 309
DB 6 FTPTVKILQSSDGGGHPPTTQLCLVSGYTPGINTIWLBDGQVMDVLDLSTATTQ 65
QY 310 GELASTQSELTLSQKHLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPFD 369
DB 66 GELASTQSELTLSQKHLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPFD 125
QY 370 LFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTVTSTLPVGT 429
DB 126 LFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTVTSTLPVGT 185
QY 430 RDMIEGETYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 489
DB 186 RDMIEGETYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245
QY 490 NFWPDISVQWLNEVQLPARSHSTTQPRKTGSGFVFVSRLEVTRAWEQKDEFICRAV 549
DB 246 NFWPDISVQWLNEVQLPARSHSTTQPRKTGSGFVFVSRLEVTRAWEQKDEFICRAV 305
QY 550 HEAAFPSQTQRAVSNVPGK 569
DB 306 HEAAFPSQTQRAVSNVPGK 325

RESULT 3
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B

us-09-701-623C-1
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match 41.6%; Score 1273.5; DB 2; Length 711;
Best Local Similarity 50.1%; Pred. No. 3.5e-99;
Matches 286; Conservative 45; Mismatches 109; Indels 131; Gaps 16;

QY 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 60
DB 236 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 295
QY 61 NNYVDGVEVHNKTKPRREQYNSTYRVISLVLTQLHONMNGKEYKKCKSNKALPAPIEKT 120
DB 296 NNYVDGVEVHNKTKPRREQYNSTYRVISLVLTQLHONMNGKEYKKCKSNKALPAPIEKT 355
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVENESNGQPNYKTTTP 180
DB 356 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVENESNGQPNYKTTTP 415
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGKL----- 468
DB 416 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGKL----- 468
QY 241 GGGSGGGSGFTPTVKILQSSCD-----GGGHFFPTIQLCLVSGYTPGINTIWLBD--- 293
DB 469 -----GGGS-----QVQLVQSGSELKKPGA-----SVKISCKASGYTFTDYGMMVWKQAPG 514
QY 294 -----GQVMDVD-----LSTASTTQEGELASTQSELTLSQKHLSDRT 331
DB 515 QGLKMGWINTVTGASTYVDDFKGPFVSLDTSVAAYLQISLKAEDT-----AT 565
QY 332 YTC-----QVYQHTFEDSTKCCADSNPRGVSAYLSRSPFDLFIKSPITICLVVDL 385
DB 566 YFCARRGFVAMYWG-----QGTIVTVSSGGGGGGGGGGSDIVLTQSPA----- 613
QY 386 AFPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTVTSTLPVTRDWISGETYQCRVTHP 445
DB 614 -----TMSASPGERV-----TLTCSASSSSISYMFYWHQRPGQS----- 646
QY 446 HLPALMRSTTK-TSGPRAAPEVYAFATPEWPGSRDKRTLACLIQFMFEDISVQWLNE 504
DB 647 --PRLLIYDTSNLASGVA-----RFGSGSGTSYSLTISRMEFEDATFYCHQS 694
QY 505 VOLPDARHSTTQPRKTGSGFFVFVRLEVTR 535
DB 695 SSVP-----FTFGQ-----TKLEIK 711

RESULT 4
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
```

```
us-09-701-623C-1
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match 41.6%; Score 1273.5; DB 2; Length 711;
Best Local Similarity 50.1%; Pred. No. 3.5e-99;
Matches 286; Conservative 45; Mismatches 109; Indels 131; Gaps 16;

QY 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 60
DB 236 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 295
QY 61 NNYVDGVEVHNKTKPRREQYNSTYRVISLVLTQLHONMNGKEYKKCKSNKALPAPIEKT 120
DB 296 NNYVDGVEVHNKTKPRREQYNSTYRVISLVLTQLHONMNGKEYKKCKSNKALPAPIEKT 355
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVENESNGQPNYKTTTP 180
DB 356 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFFPSDIAVENESNGQPNYKTTTP 415
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGKL----- 468
DB 416 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGKL----- 468
QY 241 GGGSGGGSGFTPTVKILQSSCD-----GGGHFFPTIQLCLVSGYTPGINTIWLBD--- 293
DB 469 -----GGGS-----QVQLVQSGSELKKPGA-----SVKISCKASGYTFTDYGMMVWKQAPG 514
QY 294 -----GQVMDVD-----LSTASTTQEGELASTQSELTLSQKHLSDRT 331
DB 515 QGLKMGWINTVTGASTYVDDFKGPFVSLDTSVAAYLQISLKAEDT-----AT 565
QY 332 YTC-----QVYQHTFEDSTKCCADSNPRGVSAYLSRSPFDLFIKSPITICLVVDL 385
DB 566 YFCARRGFVAMYWG-----QGTIVTVSSGGGGGGGGGGSDIVLTQSPA----- 613
QY 386 AFPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTVTSTLPVTRDWISGETYQCRVTHP 445
DB 614 -----TMSASPGERV-----TLTCSASSSSISYMFYWHQRPGQS----- 646
QY 446 HLPALMRSTTK-TSGPRAAPEVYAFATPEWPGSRDKRTLACLIQFMFEDISVQWLNE 504
DB 647 --PRLLIYDTSNLASGVA-----RFGSGSGTSYSLTISRMEFEDATFYCHQS 694
QY 505 VOLPDARHSTTQPRKTGSGFFVFVRLEVTR 535
DB 695 SSVP-----FTFGQ-----TKLEIK 711

RESULT 4
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
```


Db 2 DKTHCPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
QY 66 GVEVHNKTPREBQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKTISKAK 125
Db 62 GVEVHNKTPREBQYNSTYRVVSVLTVLHQDLNMGKEYKCKVSNKALPAPIEKTISKAK 121
QY 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 185
Db 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
QY 186 VGSFFLYSKLTVDKSRWQOQGVNFSCSVMHREALHNHYTQKSLSLSPGKVEGGSGG- 240
Db 182 DGSFFLYSKLTVDKSRWQOQGVNFSCSVMHREALHNHYTQKSLSLSPGKGGGGIEGPTLRQ 241
QY 241 -----GGSGGGGFTPTPVK 256
Db 242 WLAARAGGGGGGIEGPTLR 262

RESULT 7

US-09-422-838C-46
; Sequence 46, Application US/09422838C
; Patent No. 6835809
; GENERAL INFORMATION:
; APPLICANT: Liu, Chuan-Fa
; APPLICANT: Feige, Ulrich
; APPLICANT: Cheetham, Janet C.
; TITLE OF INVENTION: Thrombopoietic Compounds
; FILE REFERENCE: 01017/36263
; CURRENT APPLICATION NUMBER: US/09/422,838C
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,348
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-422-838C-46

Query Match 40.6%; Score 1243; DB 2; Length 269;
Best Local Similarity 88.9%; Pred. No. 3.2e-97;
Matches 232; Conservative 5; Mismatches 14; Indels 10; Gaps 1;

QY 6 DKTHCPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65
Db 2 DKTHCPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
QY 66 GVEVHNKTPREBQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKTISKAK 125
Db 62 GVEVHNKTPREBQYNSTYRVVSVLTVLHQDLNMGKEYKCKVSNKALPAPIEKTISKAK 121
QY 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 185
Db 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
QY 186 VGSFFLYSKLTVDKSRWQOQGVNFSCSVMHREALHNHYTQKSLSLSPGKVEGGSGG- 240
Db 182 DGSFFLYSKLTVDKSRWQOQGVNFSCSVMHREALHNHYTQKSLSLSPGKGGGGIEGPTLRQ 241
QY 241 -----GGSGGGGFTPTPVK 256
Db 242 WLAARAGGGGGGIEGPTLR 262

RESULT 8

US-09-181-706-8
; Sequence 8, Application US/09181706
; Patent No. 6130068
; GENERAL INFORMATION:

; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
; APPLICANT: Robert F. DuBoise, Richard S. Johnson
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,706
; FILING DATE: October 28, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/958,598 (converted to a
; APPLICATION NUMBER: Provisional, see below)
; FILING DATE: October 28, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
; APPLICATION NUMBER: conversion to Provisional application)
; FILING DATE: October 26, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-181-706-8

Query Match 40.3%; Score 1232; DB 2; Length 660;
Best Local Similarity 93.0%; Pred. No. 1e-95;
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 1 EPKSCDKTHCPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 32 DKRSCDKTHCPCPAPPEAEGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 91
QY 61 NNYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
Db 92 NNYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQDLNMGKEYKCKVSNKALPAPIEKT 151
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 152 ISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 211
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOQGVNFSCSVMHREALHNHYTQKSLSLSPGKVEGGSGG 240
Db 212 PVLDSGDSFFLYSKLTVDKSRWQOQGVNFSCSVMHREALHNHYTQKSLSLSPGK- 269
QY 241 GGS 244
Db 270 GGS 273

RESULT 9

US-09-458-791-8

```

; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 470-4189
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-066-8

Query Match 40.3%; Score 1232; DB 2; Length
Best Local Similarity 93.0%; Pred. No. 1e-95;
Matches 227; Conservative 7; Mismatches 8; Inc

Qy 1 EPKSCDKTHCTCPCPAPELLCGPSVFLPPKPKDTLMISRTPEV
Db 32 DKRSCDKTHCTCPCPAPAEAGAPSVFLPPKPKDTLMISRTPEV
Qy 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMWNGKE
Db 92 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
Qy 121 ISKAKVQPREPOVYTLTPPSRDELTKNQVSLTCLVKGFYPSDIA
Db 152 ISKAKGQPREPOVYTLTPPSREMTKNQVSLTCLVKGFYPSDIA
Qy 181 PVLDSVGSGFFLYSKLTVDKSRWQQGNFVSCSWMEALHNHYQO
Db 212 PVLDSGSGFFLYSKLTVDKSRWQQGNFVSCSWMEALHNHYQO
Qy 241 GGS 244
Db 270 GGS 273

RESULT 11
US-09-459-065-8
; Sequence 8, Application US/09459065
; Patent No. 6562949
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry

```

```

RESULT 11
US-09-459-065-8
; Sequence 8, Application US/09459065
; Patent No. 6562949
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry

```

```

; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,065
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1
; OTHER INFORMATION: /note= "Met (ATG) starts at -1"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-679-999-9

Query Match 40.2%; Score 1229; DB 2; Length 379;
Best Local Similarity 97.0%; Pred. No. 8.2e-96;
Matches 226; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 32 DKRSCDKTHTCPCPAEAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 91
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 92 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 151
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 152 ISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 211
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGKV 240
Db 212 PVLDSGSGFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK--GGGGG 269
QY 241 GGGG 244
Db 270 GGGG 273

RESULT 12
US-10-679-999-9
; Sequence 9, Application US/10679999
; Patent No. 6936439
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA

; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,065
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-459-065-8

Query Match 40.3%; Score 1232; DB 2; Length 660;
Best Local Similarity 93.0%; Pred. No. 1e-95;
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 32 DKRSCDKTHTCPCPAEAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 91
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 92 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 151
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 152 ISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 211
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGKV 240
Db 212 PVLDSGSGFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK--GGGGG 269
QY 241 GGGG 244
Db 270 GGGG 273

RESULT 13
US-09-428-082B-16
; Sequence 16, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHESTHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 253
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fc-EMP
US-09-428-082B-16

Query Match 40.1%; Score 1226; DB 2; Length 253;
Best Local Similarity 84.7%; Pred. No. 8.1e-96;
Matches 233; Conservative 7; Mismatches 11; Indels 24; Gaps 4;

Qy 6 DKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 65
Db 2 DKHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 61

Qy 66 GVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 125
Db 62 GVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 121

Qy 126 VOPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTPPVLD 185
Db 122 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTPPVLD 181

Qy 186 VGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGKGGGGSG 245
Db 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGKGGGGSG 232

Qy 246 GGSFTPTPVTKLOSSCGGHFPTIQLLCIVSG 280
Db 233 GGGTY-----SC----HFGP-LTWCKPQG 252

RESULT 14
US-08-595-043A-50
Sequence 50, Application US/08595043A
Patent No. 5915824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEULEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-50

Query Match 40.0%; Score 1225; DB 1; Length 232;
Best Local Similarity 97.0%; Pred. No. 8.7e-96;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTP 180
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTP 180

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

RESULT 15
US-09-968-362A-26
Sequence 26, Application US/09968362A
Patent No. 6797493
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
TITLE OF INVENTION: increased biological activities
FILE REFERENCE: 03SUN2001
CURRENT APPLICATION NUMBER: US/09/968,362A
CURRENT FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In version 3.1
SEQ ID NO 26
LENGTH: 232
TYPE: PRT
ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-26

Query Match 40.0%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 8.7e-96;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTP 180
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTP 180

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232

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Job time : 46 secs

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